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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:57:26 ; Search time 18 Seconds
(without alignments)
184.984 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	1	US-08-381-097A-3
2	6	100.0	6	1	US-08-381-097A-5
3	6	100.0	6	1	US-08-153-051B-4
4	6	100.0	6	1	US-08-337-684-2
5	6	100.0	6	2	US-08-151-477A-4
6	6	100.0	6	2	US-08-670-999-3
7	6	100.0	6	3	US-08-729-598-4
8	6	100.0	6	3	US-08-819-867-9
9	6	100.0	6	3	US-08-819-867-27
10	6	100.0	6	3	US-08-630-019A-1
11	6	100.0	6	3	US-09-018-545-3
12	6	100.0	6	3	US-09-114-399-3
13	6	100.0	6	4	US-09-608-636A-1
14	6	100.0	6	4	US-09-378-535-9
15	6	100.0	6	4	US-09-378-535-27
16	6	100.0	6	4	US-09-940-173A-1
17	6	100.0	6	5	PCT-US96-01206-1
18	6	100.0	7	3	US-08-729-598-8
19	6	100.0	7	4	US-09-940-173A-6
20	6	100.0	8	3	US-08-838-545-15
21	6	100.0	8	3	US-08-838-545-30
22	6	100.0	8	3	US-08-838-545-34
23	6	100.0	8	3	US-09-349-532-15
24	6	100.0	8	3	US-09-349-532-30
25	6	100.0	8	3	US-09-349-532-34
26	6	100.0	8	4	US-09-940-173A-4
27	6	100.0	9	1	US-08-337-684-3

28	6	100.0	9	3	US-08-630-019A-27	Sequence 27, Appl
29	6	100.0	9	3	US-09-069-434-14	Sequence 14, Appl
30	6	100.0	9	3	US-08-838-545-16	Sequence 16, Appl
31	6	100.0	9	3	US-09-349-532-16	Sequence 16, Appl
32	6	100.0	10	1	US-08-192-300-18	Sequence 18, Appl
33	6	100.0	10	2	US-08-531-743-10	Sequence 10, Appl
34	6	100.0	10	3	US-08-630-019A-8	Sequence 8, Appl
35	6	100.0	10	3	US-08-838-545-7	Sequence 7, Appl
36	6	100.0	10	3	US-08-838-545-11	Sequence 11, Appl
37	6	100.0	10	3	US-08-838-545-17	Sequence 17, Appl
38	6	100.0	10	3	US-08-838-545-21	Sequence 21, Appl
39	6	100.0	10	3	US-08-838-545-29	Sequence 29, Appl
40	6	100.0	10	3	US-08-974-549A-527	Sequence 527, App
41	6	100.0	10	3	US-09-349-532-7	Sequence 7, Appl
42	6	100.0	10	3	US-09-349-532-11	Sequence 11, Appl
43	6	100.0	10	3	US-09-349-532-17	Sequence 17, Appl
44	6	100.0	10	3	US-09-349-532-21	Sequence 21, Appl
45	6	100.0	10	3	US-09-349-532-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-381-097A-3
; Sequence 3, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; TITLE OF INVENTION: of Cancer and Other Diseases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: ummc 63092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

Db 1 TTAGGG 6
|||||

RESULT 2

US-08-381-097A-5/c
; Sequence 5, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
; APPLICANT: Iverson, Patrick L.
; APPLICANT: Mata, John E.
; TITLE OF INVENTION: Synthetice Oligodeoxyribonucleotides
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
; TITLE OF INVENTION: of Cancer and Other Diseases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
; STREET: 801 Grand Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,097A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: ummc 63092
; TELEPHONE: 515-288-3667
; TELEFAX: 515-288-1338
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-097A-5

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 6 TTAGGG 1
|||||

RESULT 3

US-08-153-051B-4/c
; Sequence 4, Application US/08153051B
; Patent No. 5645986
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,051B
; FILING DATE: No. 5645986ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 204/195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-153-051B-4

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 6 TTAGGG 1
|||||

RESULT 4

US-08-337-684-2
; Sequence 2, Application US/08337684
; Patent No. 5686306
; GENERAL INFORMATION:
; APPLICANT: West, Michael David
; APPLICANT: Shay, Jerry
; APPLICANT: Wright, Woodring E.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR
; TITLE OF INVENTION: MEASURING TELOMERES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: US/08/337,684
APPLICATION NUMBER: US/08/337,684
FILING DATE: No. 5686306ember 10, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,477
FILING DATE: No. 5686306ember 12, 1993
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 5686306ember 12, 1993
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-684-2

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 5
US-08-151-477A-4/c
Sequence 4, Application US/08151477A
Patent No. 5830844
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,477A
FILING DATE: No. 5830644ember 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-151-477A-4

Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 6
US-08-670-999-3
Sequence 3, Application US/08670999
Patent No. 5849727
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
APPLICANT: Iverson, Patrick L.
TITLE OF INVENTION: Compositions and Methods for Altering
TITLE OF INVENTION: the Biodistribution of Biological Agents
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,999
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: unmc 107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO

ANTI-SENSE: YES
US-08-670-999-3

Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 7

US-08-729-598-4
; Sequence 4, Application US/08729598
; Patent No. 6001657
; GENERAL INFORMATION:
; APPLICANT: Hardin, Charles C.
; APPLICANT: Brown II, Bernard A.
; APPLICANT: Roberts, John J.
; APPLICANT: Pelsue, Stephen A.
; TITLE OF INVENTION: Antibodies That Selectively Bind
; TITLE OF INVENTION: Quadruplex Nucleic Acids
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sorofini J. Biswas
; STREET: P.O. Box 37428
; CITY: Raleigh
; STATE: No. 6001657th Carolina
; COUNTRY: USA
; ZIP: 27627

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,598
FILING DATE: 11-OCT-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Biswas, Sorofini J.
REGISTRATION NUMBER: 39,111
REFERENCE/DOCKET NUMBER: 5051-301A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 854-1400
TELEFAX: (919) 854-1401
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant

MOLECULE TYPE: DNA (genomic)
US-08-729-598-4

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 8

US-08-819-867-9
; Sequence 9, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich

APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. Meeachern
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 6007989ember 12, 1993
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-9

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 9

US-08-819-867-27/c
; Sequence 27, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Meeachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn

APPLICANT: Nam Woo Kim
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 600799 September 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-27

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 10
US-08-630-019A-1
Sequence 1, Application US/08G30019A
Patent No. 6015710
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: Corey, David
APPLICANT: No. 6015710, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-JUN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-1

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 11
US-09-018-545-3
Sequence 3, Application US/09018545
Patent No. 6087493
GENERAL INFORMATION:
APPLICANT: Wheelhouse, Richard T.
APPLICANT: Hurley, Laurence H.
TITLE OF INVENTION: PORPHYRIN COMPOUNDS AS TELOMERASE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,545
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,295
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UT5B:654

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-018-545-3

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTAGGG 6

RESULT 12
US-09-114-399-3
Sequence 3, Application US/09114399
Patent No. 6245747
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
APPLICANT: Iversen, Patrick L.
APPLICANT: Meyer, Gary D.
TITLE OF INVENTION: Targeted Site Specific Drug Delivery
TITLE OF INVENTION: Compositions and Method of Use
FILE REFERENCE: 0450-0310.31
CURRENT APPLICATION NUMBER: US/09/114,399
CURRENT FILING DATE: 1998-07-13
PRIOR APPLICATION NUMBER: US 08/615,495
PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PS-ODN
US-09-114-399-3

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Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
US-09-608-636A-1
Sequence 1, Application US/09608636A
Patent No. 6518268
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Kyowa Hakko Kogyo Co., Ltd.
APPLICANT: Chin, Allison C.
APPLICANT: Holcomb, Ryan C.
APPLICANT: Piatyszek, Mieczyslaw A
APPLICANT: Singh, Upinder
APPLICANT: Tolman, Richard L.
APPLICANT: Akama, Tsutomu
APPLICANT: Kanda, Yutaka
APPLICANT: Asai, Akira
APPLICANT: Yamashita, Yoshinori
APPLICANT: Endo, Kaori
APPLICANT: Yamaguchi, Hiroyuki
TITLE OF INVENTION: Telomerase Inhibitors and Methods of Their Use

FILE REFERENCE: 055/003
CURRENT APPLICATION NUMBER: US/09/608,636A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/142,173
PRIOR FILING DATE: 1999-07-10
PRIOR APPLICATION NUMBER: JP 11-187616
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: JP 11-307576
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
US-09-608-636A-1

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTAGGG 6

RESULT 14
US-09-378-535-9
Sequence 9, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Meeachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
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; TOPOLOGY: linear
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US-09-378-535-9

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTAGGG 6

RESULT 15
US-09-378-535-27/c
; Sequence 27, Application US/09378535
; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. Mceachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-09-378-535-27

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 TTAGGG 1

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Job time : 18 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:38:14 ; Search time 380.903 Seconds
(without alignments)
682.741 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

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2: gb_htg:*

3: gb_in:*

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	6	100.0	6	6	AX058275	Sequence
C 3	6	100.0	6	6	AX175285	Sequence
C 4	6	100.0	6	6	AX268763	Sequence
C 5	6	100.0	6	6	AX268764	Sequence
C 6	6	100.0	8	6	BD230086	Method fo
C 7	6	100.0	8	6	BD071049	Modulatio
C 8	6	100.0	8	6	BD071063	Modulatio
C 9	6	100.0	8	6	BD071067	Modulatio
C 10	6	100.0	9	6	BD071050	Modulatio
C 11	6	100.0	10	6	AR026485	Sequence
C 12	6	100.0	10	6	BD238638	Preparati
C 13	6	100.0	10	6	BD238940	Preparati
C 14	6	100.0	10	6	BD239195	Preparati
C 15	6	100.0	10	6	BD240276	Preparati
C 16	6	100.0	10	6	E36980	Human telom
C 17	6	100.0	10	6	AR243501	Sequence
C 18	6	100.0	10	6	AR336866	Sequence
C 19	6	100.0	10	6	AR390657	Sequence
C 20	6	100.0	10	6	AR393271	Sequence
C 21	6	100.0	10	6	AX152177	Sequence
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C 23	6	100.0	10	6	AX153382	Sequence
C 24	6	100.0	10	6	AX153383	Sequence
C 25	6	100.0	10	6	AX153524	Sequence
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C 27	6	100.0	10	6	AX810562	Sequence
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C 29	6	100.0	10	6	BD023724	Method fo
C 30	6	100.0	10	6	BD071041	Modulatio
C 31	6	100.0	10	6	BD071045	Modulatio
C 32	6	100.0	10	6	BD071051	Modulatio
C 33	6	100.0	10	6	BD071054	Modulatio
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C 38	6	100.0	11	6	AR026486	Sequence
C 39	6	100.0	11	6	AR026487	Sequence
C 40	6	100.0	11	6	AR059195	Sequence
C 41	6	100.0	11	6	AR075506	Sequence
C 42	6	100.0	11	6	AR161904	Sequence
C 43	6	100.0	11	6	I31749	Sequence 2
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ALIGNMENTS

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DEFINITION Sequence 5 from Patent WO0073420.
ACCESSION AX055801
VERSION AX055801.1 GI:12228914
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX055801 Sequence 5 from Patent WO0073420.
AX055801
AX055801.1 GI:12228914
synthetic construct
artificial sequences.
1 (bases 1 to 6)
Hahn, W.C. and Weinberg, R.A.
Creation of human tumorigenic cells and uses therefor
Patent: WO 0073420-A 5 07-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER

6 bp DNA linear PAT 13-JAN-2001

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  DEFINITION Sequence 10 from Patent WO0074667.
  ACCESSION AX058275
  VERSION AX058275.1 GI:12310774
  KEYWORDS
  SOURCE synthetic construct
  ORGANISM synthetic construct
  REFERENCE 1
  AUTHORS Au, J. L. and Wientjes, G.
  TITLE Compositions active in telomere damage comprising a taxane and
  JOURNAL telomerase inhibitor
  Patent: WO 0074667-A 10 14-DEC-2000;
  Au, Jessie L.S. (US) ; Wientjes, Guillaume (US)
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RESULT 3
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  DEFINITION Sequence 49 from Patent WO0144465.
  ACCESSION AX175285
  VERSION AX175285.1 GI:14598653
  KEYWORDS
  SOURCE synthetic construct
  ORGANISM synthetic construct
  REFERENCE 1 (bases 1 to 6)
  AUTHORS Phillips, N.C. and Pillon, M.C.
  TITLE Therapeutically useful synthetic oligonucleotides
  JOURNAL Patent: WO 0144465-A 49 21-JUN-2001;
  Bioniche Life Sciences Inc. (CA)
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  DEFINITION Sequence 11 from Patent WO0174342.
  ACCESSION AX268763
  VERSION AX268763.1 GI:16541835
  KEYWORDS
  SOURCE synthetic construct
  ORGANISM synthetic construct
  REFERENCE 1
  AUTHORS Gilchrist, B.A., Yaar, M. and Eller, M.
  TITLE Use of locally applied dna fragments
  JOURNAL Patent: WO 0174342-A 11 11-OCT-2001;
  TRUSTEES OF BOSTON UNIVERSITY (US)
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  QY 1 TTAGGG 6
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  ACCESSION AX268764
  VERSION AX268764.1 GI:16541836
  KEYWORDS
  SOURCE synthetic construct
  ORGANISM synthetic construct
  REFERENCE 1
  AUTHORS Gilchrist, B.A., Yaar, M. and Eller, M.
  TITLE Use of locally applied dna fragments
  JOURNAL Patent: WO 0174342-A 12 11-OCT-2001;
  TRUSTEES OF BOSTON UNIVERSITY (US)
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RESULT 6
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DEFINITION Method for making complementary oligonucleotide tag sets.
ACCESSION  BD230086
VERSION    BD230086.1  GI:33039856
KEYWORDS  JP 2002528137-A/3.
SOURCE    synthetic construct
ORGANISM  synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 8)
           Williams,S.R., Kirchner,J.J. and Dubridge,R.B.
           Method for making complementary oligonucleotide tag sets
           Patent: JP 2002528137-A 3 03-SEP-2002;
           LYNX THERAPEUTICS INC
COMMENT    OS Artificial Sequence
           PN JP 2002528137-A/3
           PD 03-SEP-2002
           PF 01-NOV-1999 JP 2000579783
           PR 02-NOV-1998 US 60/106662
           PI STEVEN R WILLIAMS,JAMES J KIRCHNER,ROBERT B DUBRIDGE PC
           C12N15/09,C12N15/09,C12N11/00,C12Q1/68,C12N15/00,C12N15/00 CC
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QY      1 TTAGGG 6
Db      3 TTAGGG 8

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LOCUS      BD071049                8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION  BD071049
VERSION    BD071049.1  GI:22616652
KEYWORDS  JP 2001517929-A/15.
SOURCE    unidentified
ORGANISM  unidentified
           unclassified.
REFERENCE  1 (bases 1 to 8)
           Shay,J.W., Wright,W.E., Piatsyzek,M.A., Corey,D. and Norton,J.C.
           Modulation of mammalian telomerase by peptide nucleic acids
           Patent: JP 2001517929-A 15 09-OCT-2001;
           GERON CORP
COMMENT    OS Unidentified
           PN JP 2001517929-A/15
           PD 09-OCT-2001
           PF 09-APR-1997 JP 1997536487
           PR 09-APR-1996 US 08/630019
           PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
           PI COREY,
           PI JAMES C NORTON
           PC C07K14/00,A61K38/16,C12Q1/68
           CC Strandedness: Single;
           CC Topology: Linear;
           CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
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Best Local Similarity 100.0%; Pred. No. 5.4e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      3 TTAGGG 8

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DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION  BD071063
VERSION    BD071063.1  GI:22616666
KEYWORDS  JP 2001517929-A/29.
SOURCE    unidentified
ORGANISM  unidentified
           unclassified.
REFERENCE  1 (bases 1 to 8)
           Shay,J.W., Wright,W.E., Piatsyzek,M.A., Corey,D. and Norton,J.C.
           Modulation of mammalian telomerase by peptide nucleic acids
           Patent: JP 2001517929-A 29 09-OCT-2001;
           GERON CORP
COMMENT    OS Unidentified
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           PD 09-OCT-2001
           PF 09-APR-1997 JP 1997536487
           PR 09-APR-1996 US 08/630019
           PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
           PI COREY,
           PI JAMES C NORTON
           PC C07K14/00,A61K38/16,C12Q1/68
           CC Strandedness: Single;
           CC Topology: Linear;
           CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
           linkages are replaced by N-(2-aminoethyl)glycine units linked
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           methylenecarbonyl linker'.
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Best Local Similarity 100.0%; Pred. No. 5.4e+09;
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LOCUS      BD071067      8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION  BD071067
VERSION    BD071067.1  GI:22616670
KEYWORDS   JP 2001517929-A/33.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 8)
AUTHORS    Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
TITLE      Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL    Patent: JP 2001517929-A 33 09-OCT-2001;
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COMMENT    OS      Unidentified
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          PD      09-OCT-2001
          PF      09-APR-1997 JP 1997536487
          PR      09-APR-1996 US 08/630019
          PI      JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
          PJ      COREY,
          PK      JAMES C NORTON
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          VERSION    AR026485.1  GI:5937325
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          ORGANISM   Unclassified.
          REFERENCE  1 (bases 1 to 10)
          AUTHORS    Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
          TITLE      Rapid and sensitive assays for detecting and distinguishing between
          JOURNAL    progressive and non-processive telomerase activities
          PATENT     Patent: US 5856096-A 10 05-JAN-1999;
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          ACCESSION  BD238638
          VERSION    BD238638.1  GI:33048408
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          SOURCE     Homo sapiens (human)
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          PD      09-OCT-2001
          PF      09-APR-1997 JP 1997536487
          PR      09-APR-1996 US 08/630019
          PI      JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
          PJ      COREY,
          PK      JAMES C NORTON
          PC      C07K14/00,A61K38/16,C12Q1/68
          CC      Strandedness: Single;
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          CC      phosphate
          CC      linkages are replaced by N-(2-aminoethyl)glycine units linked
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          CC      nucleotide bases via glycine amino N through a CC
          CC      methylenecarbonyl linker'
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          ACCESSION  BD071050
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          KEYWORDS   JP 2001517929-A/16.
          SOURCE     unidentified
          ORGANISM   unidentified
          REFERENCE  1 (bases 1 to 9)
          AUTHORS    Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
          TITLE      Modulation of mammalian telomerase by peptide nucleic acids
          JOURNAL    Patent: JP 2001517929-A 16 09-OCT-2001;
          GERON CORP
          COMMENT    OS      Unidentified

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 56 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/56
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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VERSION BD239195.1 GI:33048965
KEYWORDS JP 2002534056-A/613.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 613 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/613
PD 15-OCT-2002
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ACCESSION BD238940
VERSION BD238940.1 GI:33048710
KEYWORDS JP 2002534056-A/358.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 358 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/358
PD 15-OCT-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCES
1 (bases 1 to 10)
Authors: Roberts, B.L. and Shankara, S.
Title: Preparation and use of superior vaccines
Patent: JP 2002534056-A 1694 15-OCT-2002;
JOURNAL GENZYME CORP
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Maximum Match 100%

Listing first 45 summaries

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8: Geneseq2003bs.*

9: Geneseq2003cs.*

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5	6	100.0	6	6 ABN73654	Abn73654 Bovine em
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8	6	100.0	7	1 AAN91439	Aan91439 Telomere
9	6	100.0	7	1 AAN91442	Aan91442 Variant o
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23	6	100.0	9	4 AAS15437	Aas15437 PNA 29 in

C 24	6	100.0	9	6 ABK87319	Abk87319 Drosophil
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29	6	100.0	10	2 AAV07770	Aav07770 N3 to P5
C 30	6	100.0	10	2 AAV41382	Aav41382 Antisense
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32	6	100.0	10	2 AAX21995	Aax21995 Telomere
C 33	6	100.0	10	2 AAX28358	Aax28358 Lung canc
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35	6	100.0	10	2 AAX277628	Aax277628 Human den
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37	6	100.0	10	3 AAZ79266	Aaz79266 Human den
38	6	100.0	10	3 AAZ78185	Aaz78185 Human den
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ALIGNMENTS

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ID AAT05734 standard; DNA; 6 BP.

XX

AC AAT05734;

XX

DT 01-FEB-1996 (first entry)

XX Telomerase oligonucleotide substrate #1.

DE Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;

KW transplanted; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.

XX Synthetic.

OS WO9513383-A1.

EN 18-MAY-1995.

XX 10-NOV-1994; 94WO-US013130.

XX 12-NOV-1993; 93US-00151477.

PR 12-NOV-1993; 93US-00153051.

XX (GERO-) GERON CORP.

PA (TEXA) UNIV TEXAS SYSTEM.

XX Shay J, West MD, Wright WE;

XX WPI; 1995-224051/29.

XX Increasing telomere length in cells - to increase proliferative capacity

PT and therefore delay cellular senescence, useful in cell therapy and

PT transplanted.

XX Claim 12; Page 29; 38pp; English.

XX Oligonucleotides AAT05734-7 are examples of telomerase substrates used to

CC increase the proliferative capacity of normal cells that express

CC telomerase activity. The oligonucleotides allow an increase in length of

CC telomeres in normal cells and in hybrids of normal and immortalised

CC cells. The increase in telomere length extends the capacity of cells to

CC replicate, esp. those treated ex vivo and used for transplantation

CC techniques e.g. cell therapy, for the treatment of AIDS, anaemia,

CC leukaemia or lymphoma

XX

SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 6; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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 ID AAX80998 standard; DNA; 6 BP.
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 AC
 XX
 XX
 DT 13-SEP-1999 (first entry)
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 DE Telomeric repeat sequence.
 XX
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 KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
 KW immunogen; enzyme; telomerase-mediated DNA replication; human; ss.
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 OS Homo sapiens.
 XX
 PN WO927113-A1.
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 PD 03-JUN-1999.
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 PF 25-NOV-1998; 98WO-US025211.
 XX
 PR 26-NOV-1997; 97US-00979742.
 PR 16-MAR-1998; 98US-00042460.
 XX
 PA (GERO-) GERON CORP.
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX
 XX Morin GB, Allsopp R, Depinho R, Greenberg R;
 PI WPI; 1999-347722/29.
 DR
 XX
 XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
 PT nucleic acids.
 XX
 PS Disclosure; Page 62; 135pp; English.
 CC
 CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
 CC enzyme. Compositions containing mTERT can be used in telomere length
 CC assays. Isolated mTERT is useful as an immunogen for the production of
 CC monoclonal or polyclonal antibodies. The method is useful for assessing
 CC the degree of purification and identification of new mTERT species, such
 CC as an mTERT allele, homolog or isoform, or to screen for modulators
 CC (antagonists and agonists) of telomerase-mediated DNA replication.
 CC Antagonists and agonists of mTERT can be used to modify the activity of
 CC other telomerase enzymes such as human TERT (hTERT)
 CC
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 SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
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 ID AAS14916 standard; DNA; 6 BP.
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 AC AAS14916;

14-FEB-2002 (first entry)
 Melanogenesis associated oligonucleotide #12.
 Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
 tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 conjunctivitis; allergic rhinitis; vitiligo; ss.
 Synthetic.
 WO200174342-A2.
 11-OCT-2001.
 30-MAR-2001; 2001WO-US010162.
 31-MAR-2000; 2000US-00540843.
 (UYBO-) UNIV BOSTON.
 Gilchrest BA, Year M, Eller M;
 WPI; 2001-626338/72.
 Inhibiting proliferation of epithelial cells, useful e.g. for treating
 carcinoma, using specific oligonucleotides that mimic the effects of
 ultra-violet light.
 Claim 1; Page 37; 74pp; English.
 The invention describes inhibition of mammalian epithelial cell
 proliferation by treating cells with at least one oligonucleotide, or its
 fragment. The compounds, which have cytostatic, anti-allergic, anti-
 inflammatory, dermatological, ophthalmological, anti-psoriatic and
 immunosuppressive activities, function as 'ultra-violet mimics' to induce
 DNA repair processes (or a protective response to later exposure to
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 or a tumour necrosis factor inhibitor. Probably they mimic products of
 DNA damage, or processed DNA-damage intermediates, by inducing the p53
 pathway, resulting in transient arrest of cell growth, allowing more time
 for DNA repair to occur before cell division takes place. The method is
 especially used to treat carcinoma but may also be used to: treat other
 hyperproliferative states (e.g. psoriasis or precancerous conditions);
 reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
 allergically mediated inflammation (atopic or contact dermatitis,
 allergic rhinitis and conjunctivitis); prevent or reduce melanin production
 cells caused by radiation or chemicals; increase melanin production
 (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 promote apoptosis in epithelial cells that contain damaged DNA. Also
 oligonucleotides that contain non-hydrolyzable backbones are used to
 inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 sequence is melanogenesis associated oligonucleotide #12, the reverse
 complementary sequence of AAS149015, a truncated version of the sequence
 representing the telomere over-hang sequence (AAS14909), described in the
 method of the invention
 Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 100.0%; Score 6; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTAGGG 6
 |||||
 Db 6 TTAGGG 1

RESULT 4
 AAS14915

KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;
KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;
KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;
KW gp-1100; hyperproliferative disorder; spongiosis; blistering;
KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;
KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;
KW atopic dermatitis; breast cancer; lung cancer; liver cancer;
KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;
KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;
KW stomach cancer; thyroid cancer.
XX
XX
OS Homo sapiens.
XX
XX US2003032610-A1.
XX
XX 13-FEB-2003.
XX
XX 12-APR-2002; 2002US-00122630.
XX
XX 03-JUN-1996; 96WO-US008386.
XX 26-MAR-1998; 98US-00048927.
XX 31-MAR-2000; 2000US-00540843.
XX 30-MAR-2001; 2001WO-US010162.
XX
XX (GILC/) GILCHREST B A.
XX PA (ELLE/) ELLER M S.
XX PA (YAAR/) YAAR M.
XX
XX Gilchrest BA, Eller MS, Yaar M;
XX WPI; 2003-512221/48.
XX
XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,
XX PT by administering composition having oligonucleotides that share sequence
XX PT identity with human telomere overhang repeat.
XX
XX Claim 44; Page 9; 65pp; English.
XX
XX The invention relates to inhibiting growth of cancer cells, which is
XX independent of presence or activity of telomerase in cells, not requiring
XX the presence or activity of p53 normal function in cells, or resulting in
XX S-phase arrest in cells, and inducing apoptosis in cancer cells,
XX involving administering a composition comprising oligonucleotides which
XX share at least 50% sequence identity with human telomere overhang repeat,
XX (TTAGG)n. The composition may contain 2 of the oligonucleotides for their
XX contiguous portion) and is used in a method inhibiting proliferation of
XX epithelial cells in a mammal or preventing/reducing DNA damage in cells
XX of a mammal, where the DNA damage is caused by radiation or DNA-damaging
XX chemicals. The method is useful for inhibiting growth of cancer cells
XX (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,
XX squamous cell carcinoma), for inducing apoptosis in cancer cells in
XX human, promoting differentiation of malignant cells in a mammal,
XX enhancing the expression of one or more surface antigens (e.g. MART-1,
XX tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer
XX cells (especially melanoma cells) in a human and for treatment of other
XX hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis
XX in the skin of a mammal, skin cancer in a human with xeroderma
XX pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or
XX basal cell carcinoma) and for treating or preventing pre-cancerous
XX conditions affecting epithelial cells (such as psoriasis and atopic
XX dermatitis) and also the types of cancers of breast, lung, liver,
XX prostate, pancreatic, ovarian, bladder, uterine, colon, brain,
XX oesophagus, stomach, and thyroid. The present sequence is the telomere
XX repeat unit sequence
XX
XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 6; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
|||||

Db 1 TTAGGG 6
RESULT 7
ACD25831/C
ID ACD25831 standard; DNA; 6 BP.
XX
XX ACD25831;
AC
XX 08-SEP-2003 (first entry)
DT
XX
XX Telomere repeat unit (complement).
DE
XX
XX Telomere; ds; Cytostatic; human; antipsoriatic; dermatological;
KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;
KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;
KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;
KW gp-1100; hyperproliferative disorder; spongiosis; blistering;
KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;
KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;
KW atopic dermatitis; breast cancer; lung cancer; liver cancer;
KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;
KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;
KW stomach cancer; thyroid cancer.
XX
XX Homo sapiens.
OS
XX
XX US2003032610-A1.
XX
XX 13-FEB-2003.
XX
XX 12-APR-2002; 2002US-00122630.
XX
XX 03-JUN-1996; 96WO-US008386.
XX 26-MAR-1998; 98US-00048927.
XX 31-MAR-2000; 2000US-00540843.
XX 30-MAR-2001; 2001WO-US010162.
XX
XX (GILC/) GILCHREST B A.
XX PA (ELLE/) ELLER M S.
XX PA (YAAR/) YAAR M.
XX
XX Gilchrest BA, Eller MS, Yaar M;
XX WPI; 2003-512221/48.
XX
XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,
XX PT by administering composition having oligonucleotides that share sequence
XX PT identity with human telomere overhang repeat.
XX
XX Claim 44; Page 18; 65pp; English.
XX
XX The invention relates to inhibiting growth of cancer cells, which is
XX independent of presence or activity of telomerase in cells, not requiring
XX the presence or activity of p53 normal function in cells, or resulting in
XX S-phase arrest in cells, and inducing apoptosis in cancer cells,
XX involving administering a composition comprising oligonucleotides which
XX share at least 50% sequence identity with human telomere overhang repeat,
XX (TTAGG)n. The composition may contain 2 of the oligonucleotides for their
XX contiguous portion) and is used in a method inhibiting proliferation of
XX epithelial cells in a mammal or preventing/reducing DNA damage in cells
XX of a mammal, where the DNA damage is caused by radiation or DNA-damaging
XX chemicals. The method is useful for inhibiting growth of cancer cells
XX (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,
XX squamous cell carcinoma), for inducing apoptosis in cancer cells in
XX human, promoting differentiation of malignant cells in a mammal,
XX enhancing the expression of one or more surface antigens (e.g. MART-1,
XX tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer
XX cells (especially melanoma cells) in a human and for treatment of other
XX hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis
XX in the skin of a mammal, skin cancer in a human with xeroderma
XX pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or
XX basal cell carcinoma) and for treating or preventing pre-cancerous

CC conditions affecting epithelial cells (such as psoriasis and atopic dermatitis) and also the types of cancers of breast, lung, liver, CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain, CC oesophagus, stomach, and thyroid. The present sequence is the complement CC of telomere repeat unit sequence found to be less active in melanogenesis XX

SQ Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 8

AA091439/c
ID AA091439 standard; DNA; 7 BP.

XX AC AA091439;

XX DT 25-MAR-2003 (revised)
XX DT 22-FEB-1990 (first entry)

XX DE Telomere of Arabidopsis thaliana.

XX KW Telomere; Arabidopsis thaliana; vector; artificial chromosomes;
XX KW tandem repeat.

XX OS Arabidopsis thaliana.

XX PN W08909219-A.

XX PD 05-OCT-1989.

XX PF 27-FEB-1989; 89WO-US000795.

XX PR 24-MAR-1988; 88US-00172467.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Richards E, Ausubel FM;

XX DR WPI; 1989-309497/42.

XX PT New recombinant DNA contg. eukaryotic telomere esp. from higher plant -
XX PT useful as vector for specific genes and maintained in nucleus as
XX PT independent replicating molecule.

XX PS Claim 28; Page 50; 65pp; English.

XX CC Tandem repeats (1-1000) of the telomere are used in a vector for
XX CC expressing specific genes in plants. They provide 'artificial
XX CC chromosomes' which are maintained in the nucleus, so are not subjected to
XX CC variable expression due to integration-position effects. They allow the
XX CC integration of very foreign DNA without host range limitations. The
XX CC telomere opt. contains variant repeats of CTCAAA. The telomere is pref.
XX CC the pAT4 plasmid (ATCC 67577). (Updated on 25-MAR-2003 to correct PA
XX CC field.)

XX SQ Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 9

AA091442/c

ID AA091442 standard; DNA; 7 BP.

XX AC AA091442;

XX DT 25-MAR-2003 (revised)
XX DT 22-FEB-1990 (first entry)

XX DE Variant of Arabidopsis thaliana telomere.

XX KW Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
XX KW tandem repeat.

XX OS Arabidopsis thaliana.

XX PN W08909219-A.

XX PD 05-OCT-1989.

XX PF 27-FEB-1989; 89WO-US000795.

XX PR 24-MAR-1988; 88US-00172467.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Richards E, Ausubel FM;

XX DR WPI; 1989-309497/42.

XX PT New recombinant DNA contg. eukaryotic telomere esp. from higher plant -
XX PT useful as vector for specific genes and maintained in nucleus as
XX PT independent replicating molecule.

XX PS Claim 35; Page 50; 65pp; English.

XX CC The DNA is a variant of the telomere of the pAT4 plasmid (ATCC 67577).
XX CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 10

AA097993

ID AA097993 standard; DNA; 8 BP.

XX AC AA097993;

XX DT 25-MAR-2003 (revised)
XX DT 19-OCT-1995 (first entry)

XX DE Peptide nucleic acid oligomer targetting HIV gene.

XX KW Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
XX KW antiviral; antisense; triple helix; ss.

XX OS Synthetic.

XX PH Key misc_feature Location/Qualifiers
XX FT 1. .8

XX FT /note= "at least one (and preferably all) of the backbone
XX FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine
XX FT peptide residues, the nucleobase being attached
XX FT covalently to the acetyl group and the peptide linkage

PR 09-APR-1996; 96US-00630019.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Wright WE, Piatsyzek MA, Shay JW, Norton JC, Corey DR;
 XX WPI; 2000-292432/25.
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase activity
 PT in mammalian cells is useful as probes to detect the RNA component of a
 PT mammalian telomerase.
 PS Claim 6; Col 71; 45pp; English.
 XX The present sequence represents a peptide nucleic acid molecule which
 CC hybridizes to the mRNA component of mammalian telomerase, and inhibits
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that
 CC synthesizes one strand of the telomeric DNA, using as a template an 11
 CC nucleotide sequence contained within the RNA component of the enzyme. The
 CC invention relates to PNA molecules having a sequence of no more than 25
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytoskeletal agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component
 XX Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 6; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTAGGG 6
 Db |||||
 2 TTAGGG 7
 RESULT 13
 AAA37572/c
 ID AAA37572 standard; DNA; 8 BP.
 AC AAA37572;
 XX 15-AUG-2000 (first entry)
 DE PNA sequence #30 used to inhibit telomerase activity.
 XX Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ss.
 XX Synthetic.
 OS
 XX

FH Key Location/Qualifiers
 FT misc_feature 1..8
 FT /*tag= a
 FT /note= "Peptide nucleic acid molecule, where N-(2-
 FT aminoethyl)glycine units are linked to nucleotide bases
 FT via glycine amino N through a methylene-carbonyl linker"
 XX
 PN US6046307-A.
 XX 04-APR-2000.
 XX 09-APR-1997; 97US-00838545.
 XX 09-APR-1996; 96US-00630019.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Wright WE, Piatsyzek MA, Shay JW, Norton JC, Corey DR;
 XX WPI; 2000-292432/25.
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase activity
 PT in mammalian cells is useful as probes to detect the RNA component of a
 PT mammalian telomerase.
 PS Example 2; Col 33; 45pp; English.
 XX The present sequence represents a peptide nucleic acid molecule which
 CC hybridizes to the mRNA component of mammalian telomerase, and inhibits
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that
 CC synthesizes one strand of the telomeric DNA, using as a template an 11
 CC nucleotide sequence contained within the RNA component of the enzyme. The
 CC invention relates to PNA molecules having a sequence of no more than 25
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytoskeletal agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component
 XX Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 100.0%; Score 6; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTAGGG 6
 Db |||||
 7 TTAGGG 2
 RESULT 14
 AAS15436
 ID AAS15436 standard; DNA; 8 BP.
 XX

AC AAS15436;
 XX DT 14-FEB-2002 (first entry)
 XX DE PNA 28 inhibiting human and mammalian telomerase activity.
 XX
 KW Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
 KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
 KW inflammation; lymphoproliferative disease; autoimmune disease;
 KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;
 KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
 KW immunosuppressive; polyamide backbone; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..8
 FT /tag= a
 FT /note= "This sequence is a peptide nucleic acid, i.e. it
 FT contains a polyamide backbone instead of a deoxyribose
 FT backbone"
 XX
 PN US6294650-B1.
 XX
 XX 25-SEP-2001.
 XX
 XX 08-JUL-1999; 99US-00349532.
 XX
 PR 09-APR-1996; 96US-00630019.
 PR 09-APR-1997; 97US-00838545.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;
 XX WPI; 2001-638024/73.
 DR
 XX New peptide nucleic acids that hybridizes to the RNA component of
 FT mammalian telomerase, useful for treating or preventing cancer,
 FT inflammation, lymphoproliferative diseases, autoimmune disease, or
 FT neurodegenerative diseases.
 XX
 PS Claim 7; Col 73; 46pp; English.
 XX
 XX The present invention relates to peptide nucleic acids (PNAs), comprising
 CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
 CC mammalian cells by hybridising to the RNA component of mammalian
 CC telomerase. The PNAs are useful as probes to detect the RNA component of
 CC mammalian telomerase and as inhibitors of telomerase activity, or to
 CC detect and/or quantitate polynucleotide having the human telomerase RNA
 CC component (hTR) sequence, as well as in forensic identification of
 CC individuals, such as paternity testing or identification of criminal
 CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
 CC PNA can be further used for treating or preventing cancer, inflammation,
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
 CC diseases. The PNAs in combination with other pharmaceuticals (such as
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
 CC diseases characterised by abnormal telomere metabolism or telomerase
 CC activity. The present sequence represents one of the PNA sequences of the
 CC invention
 XX
 XX Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 6; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 TTAGGG 6
 |||||

Db 2 TTAGGG 7
 RESULT 15
 AAS15474
 ID AAS15474 standard; DNA; 8 BP.
 XX
 AC AAS15474;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE PNA 34 inhibiting human and mammalian telomerase activity.
 XX
 KW Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
 KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
 KW inflammation; lymphoproliferative disease; autoimmune disease;
 KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;
 KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
 KW immunosuppressive; polyamide backbone; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..8
 FT /tag= a
 FT /note= "This sequence is a peptide nucleic acid, i.e. it
 FT contains a polyamide backbone instead of a deoxyribose
 FT backbone"
 XX
 PN US6294650-B1.
 XX
 XX 25-SEP-2001.
 XX
 XX 08-JUL-1999; 99US-00349532.
 XX
 PR 09-APR-1996; 96US-00630019.
 PR 09-APR-1997; 97US-00838545.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;
 XX WPI; 2001-638024/73.
 DR
 XX New peptide nucleic acids that hybridizes to the RNA component of
 FT mammalian telomerase, useful for treating or preventing cancer,
 FT inflammation, lymphoproliferative diseases, autoimmune disease, or
 FT neurodegenerative diseases.
 XX
 PS Claim 7; Col 73; 46pp; English.
 XX
 XX The present invention relates to peptide nucleic acids (PNAs), comprising
 CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
 CC mammalian cells by hybridising to the RNA component of mammalian
 CC telomerase. The PNAs are useful as probes to detect the RNA component of
 CC mammalian telomerase and as inhibitors of telomerase activity, or to
 CC detect and/or quantitate polynucleotide having the human telomerase RNA
 CC component (hTR) sequence, as well as in forensic identification of
 CC individuals, such as paternity testing or identification of criminal
 CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
 CC PNA can be further used for treating or preventing cancer, inflammation,
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
 CC diseases. The PNAs in combination with other pharmaceuticals (such as
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
 CC diseases characterised by abnormal telomere metabolism or telomerase
 CC activity. The present sequence represents one of the PNA sequences of the
 CC invention
 XX
 XX Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 6; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 TTAGGG 6
 |||||

CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents one of the PNA sequences of the
CC invention. Note: The present sequence is given in the SEQ ID listing but
CC is not mentioned elsewhere in the patent
XX

SQ Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 2 Other;

Query Match 100.0%; Score 6; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTAGGG 6

Db 2 TTAGGG 7

Search completed: August 11, 2004, 17:56:37
Job time : 89.043 secs

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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 19:00:04 ; Search time 86 5161 Seconds
(without alignments)
340.279 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 2263564

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Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6	100.0	6	9	US-09-817-387-29	Sequence 29, Appl
2	6	100.0	6	9	US-09-735-363A-49	Sequence 49, Appl
3	6	100.0	6	9	US-09-730-893-1	Sequence 1, Appl
4	6	100.0	6	10	US-09-940-173A-1	Sequence 1, Appl
5	6	100.0	6	13	US-09-907-279-2	Sequence 2, Appl
6	6	100.0	6	15	US-10-122-630-11	Sequence 11, Appl
7	6	100.0	6	15	US-10-122-630-11	Sequence 12, Appl
8	6	100.0	6	15	US-10-122-633-11	Sequence 11, Appl
9	6	100.0	6	15	US-10-122-633-11	Sequence 11, Appl
10	6	100.0	6	15	US-10-255-535-8	Sequence 8, Appl
11	6	100.0	6	15	US-10-336-265-1	Sequence 1, Appl
12	6	100.0	6	15	US-10-336-265-3	Sequence 3, Appl
13	6	100.0	6	15	US-10-336-265-4	Sequence 4, Appl
14	6	100.0	6	15	US-10-336-265-4	Sequence 63, Appl

15	6	100.0	6	15	US-10-336-265-64	Sequence 64, Appl
16	6	100.0	6	15	US-10-232-927A-9	Sequence 9, Appl
c 17	6	100.0	6	15	US-10-232-927A-27	Sequence 27, Appl
18	6	100.0	6	16	US-10-382-754B-3	Sequence 3, Appl
19	6	100.0	6	16	US-10-355-388-3	Sequence 3, Appl
20	6	100.0	6	17	US-10-181-823-13	Sequence 13, Appl
21	6	100.0	6	17	US-10-705-531-15	Sequence 15, Appl
22	6	100.0	6	17	US-10-705-531-15	Sequence 16, Appl
23	6	100.0	7	9	US-09-730-893-6	Sequence 6, Appl
24	6	100.0	7	10	US-09-940-173A-6	Sequence 6, Appl
25	6	100.0	8	9	US-09-730-893-4	Sequence 4, Appl
26	6	100.0	8	10	US-09-940-173A-4	Sequence 4, Appl
27	6	100.0	8	15	US-10-336-265-58	Sequence 58, Appl
c 28	6	100.0	9	9	US-09-728-574-19	Sequence 19, Appl
29	6	100.0	10	13	US-10-325-810-527	Sequence 527, App
30	6	100.0	10	14	US-10-033-145-56	Sequence 56, Appl
31	6	100.0	10	14	US-10-033-145-358	Sequence 358, App
32	6	100.0	10	14	US-10-033-145-613	Sequence 613, App
33	6	100.0	10	14	US-10-033-145-1694	Sequence 1694, Ap
34	6	100.0	10	15	US-10-044-692-294	Sequence 294, App
35	6	100.0	10	15	US-10-044-539-294	Sequence 294, App
36	6	100.0	10	15	US-10-390-045-41	Sequence 41, Appl
37	6	100.0	10	15	US-10-330-627-92	Sequence 92, Appl
c 38	6	100.0	10	15	US-10-330-627-1296	Sequence 1296, Ap
39	6	100.0	10	15	US-10-330-627-1297	Sequence 1297, Ap
c 40	6	100.0	10	15	US-10-330-627-1298	Sequence 1298, Ap
41	6	100.0	10	15	US-10-330-627-1439	Sequence 1439, Ap
42	6	100.0	10	17	US-10-434-479-41	Sequence 41, Appl
c 43	6	100.0	11	9	US-09-057-351-2	Sequence 2, Appl
44	6	100.0	11	10	US-09-835-370-63	Sequence 63, Appl
c 45	6	100.0	11	10	US-09-249-155-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-817-387-29
; Sequence 29, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: telomeric
; OTHER INFORMATION: DNA of man
US-09-817-387-29

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
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Db 1 TTAGGG 6

RESULT 2
US-09-735-363A-49
; Sequence 49, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:

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; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Miguel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-49

Query Match      100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 3
US-09-730-893-1
; Sequence 1, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: G-QUADRUPLIX-INTERACTION COMPOUND
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-730-893-1

Query Match      100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 4
US-09-940-173A-1
; Sequence 1, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
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; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: G-QUADRUPLIX-INTERACTION COMPOUND
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/730,893
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-940-173A-1

Query Match      100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 5
US-09-907-279-2
; Sequence 2, Application US/09907279
; Publication No. US20020068296A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Adam
; TITLE OF INVENTION: CATHODIC PROTECTION OF NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 11154.41USU1
; CURRENT APPLICATION NUMBER: US/09/907,279
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,959
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial oligonucleotide sequence
US-09-907-279-2

Query Match      100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 6
US-10-122-630-11
; Sequence 11, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
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; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-11

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
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Db 1 TTAGGG 6

RESULT 7
US-10-122-630-12/c
; Sequence 12, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-12

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||

Db 6 TTAGGG 1

RESULT 8
US-10-122-633-11
; Sequence 11, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-11

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 1 TTAGGG 6

RESULT 9
US-10-122-633-12/c
; Sequence 12, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-12

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 6 TTAGGG 1

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; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-3

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      6 TTAGGG 1

RESULT 13
US-10-336-265-4/c
; Sequence 4, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-336-265-4

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      6 TTAGGG 1

RESULT 14
US-10-336-265-63
; Sequence 63, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 6

; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 6

; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-1

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 11
US-10-336-265-1
; Sequence 1, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-1

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 12
US-10-336-265-3/c
; Sequence 3, Application US/10336265
; Publication No. US20030148988A1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-63

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
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Db 1 TTAGGG 6

RESULT 15

US-10-336-265-64
; Sequence 64, Application US/10336265
; Publication No. US2003014898A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NFUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-336-265-64

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.9e+08;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
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Db 1 UUAGGG 6

Search completed: August 11, 2004, 21:11:08
Job time : 87.8495 secs

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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 16:50:49 ; Search time 718.258 Seconds
(without alignments)
249.455 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 ttaggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
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9: gb_est1:*
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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gsl:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	7	6	100.0	20	28	AZ345513
	8	6	100.0	20	28	AZ627174
	9	6	100.0	20	28	AZ662909
	10	6	100.0	20	28	AZ808291
C	11	6	100.0	20	28	AZ960008
C	12	6	100.0	20	29	TA158A03P
C	13	6	100.0	20	29	TA199G02Q
C	14	6	100.0	21	10	AW248826
C	15	6	100.0	21	10	AW248836
C	16	6	100.0	21	14	CF281817
C	17	6	100.0	21	28	AZ331625
C	18	6	100.0	21	28	AZ399400
C	19	6	100.0	21	28	AZ445481
C	20	6	100.0	21	28	AZ626594
C	21	6	100.0	21	28	AZ760907
C	22	6	100.0	21	28	AZ766315
C	23	6	100.0	21	28	AZ828389
C	24	6	100.0	21	28	AZ833919
C	25	6	100.0	21	28	AZ877328
C	26	6	100.0	22	9	AA954126
C	27	6	100.0	22	9	AA527213
C	28	6	100.0	22	14	D18745
C	29	6	100.0	22	28	AZ324747
C	30	6	100.0	22	28	AZ464647
	31	6	100.0	22	28	AZ483833
	32	6	100.0	22	28	AZ500414
C	33	6	100.0	22	28	AZ598320
C	34	6	100.0	22	28	AZ629501
	35	6	100.0	22	28	AZ666649
	36	6	100.0	22	28	AZ836104
C	37	6	100.0	22	28	AZ855118
C	38	6	100.0	23	9	AU258772
C	39	6	100.0	23	14	CA794240
C	40	6	100.0	23	28	AZ423815
	41	6	100.0	23	28	AZ465280
	42	6	100.0	23	28	AZ623979
	43	6	100.0	23	28	AZ817008
C	44	6	100.0	23	28	AZ979817
	45	6	100.0	23	28	BH857265

ALIGNMENTS

RESULT 1
AW248958
LOCUS
DEFINITION
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW248958 16 bp mRNA linear EST 07-JAN-2000
2819454.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819454 3',
mRNA sequence.
AW248958
AW248958.1 GI:6591951
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NTH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819454.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LMNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone Distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LMNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross_match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQualitySequence>: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L16M1 row: K column: 7
High quality sequence stop: 15.

FEATURES

Location/Qualifiers

1..16
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:2819454"
/tissue_type="small cell carcinoma"
/cell_line="MG3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 6; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 9 TTAGGG 14

RESULT 2

AZ392246 19 bp DNA linear GSS 03-OCT-2000
LOCUS IM0154G12R Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0154G12 R, genomic survey sequence.

ACCESSION AZ392246
VERSION AZ392246.1 GI:10507234

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D., Weiss,R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0154 row: G column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19
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/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0154G12"
/sex="Male"
/lab_host="F. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 14 TTAGGG 19

RESULT 3

AZ422271/c 19 bp DNA linear GSS 03-OCT-2000
LOCUS IM0200F10R Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0200F10 R, genomic survey sequence.

ACCESSION AZ422271
VERSION AZ422271.1 GI:10546284

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D., Weiss,R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0200 row: F column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES                                     Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0200F10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 100.0%; Score 6; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
   |||||
Db 8 TTAGGG 3

RESULT 4
AZ614760
LOCUS
DEFINITION
IM043A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0443A17 R, genomic survey sequence.
ACCESSION
AZ614760
VERSION
AZ614760.1 GI:11736950
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0443 row: A column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES                                     Location/Qualifiers
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0443A17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 100.0%; Score 6; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
   |||||
Db 4 TTAGGG 9

RESULT 5
AZ826736/c
LOCUS
DEFINITION
2M0102N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102N07 R, genomic survey sequence.
ACCESSION
AZ826736
VERSION
AZ826736.1 GI:12996644
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: N column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0102N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||

Db 17 TTAGGG 12

RESULT 6

BQ593485/c
LOCUS BQ593485 20 bp mRNA linear EST 06-DRC-2002
DEFINITION S015529-024-026-P04-SP6 MPZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-026-P04 5-PRIME, mRNA sequence.
ACCESSION BQ593485
VERSION BQ593485.1 GI:26123068
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 20)
AUTHORS Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 20 Std Error: 0.00
Plate: 26 row: P column: 04
Seq primer: SP6; CATACGATTAGTGACTATAG.

FEATURES

source

Location/Qualifiers
1. .20

/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:193369"
/db_xref="taxon:161934"
/clone="024-026-P04"
/tissue_type="developing root"
/lab_host="EMOH108"
/clone_lib="MPZ-ADIS-024-developing root"
/note="Vector: PCWVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Query Match 100.0%; Score 6; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||

Db 18 TTAGGG 13

RESULT 7

AZ345513/c
LOCUS AZ345513 20 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0080J04F Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGClM0080J04 F, genomic survey sequence.
ACCESSION AZ345513
VERSION AZ345513.1 GI:10424750
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGClM0080J04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
|||||
Db 13 TTAGGG 18

RESULT 9
AZ662909
LOCUS
DEFINITION
IM0542G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0542G17 F, genomic survey sequence.
ACCESSION
AZ662909
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: G column: 17
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542G17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
|||||
Db 16 TTAGGG 11

RESULT 8
AZ627174
LOCUS
DEFINITION
IM0467010R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0467010 R, genomic survey sequence.
ACCESSION
AZ627174
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: O column: 10
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467010"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6

Db 7 TTAGGG 12

RESULT 10

AZ808291

LOCUS

DEFINITION AZ808291 20 bp DNA linear GSS 20-FEB-2001
 clone UUGC2M0071D09 R, genomic survey sequence.

ACCESSION AZ808291

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0071 row: D column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0071D09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

FEATURES

source

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0227G21"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6

Db 6 TTAGGG 11

RESULT 11

AZ960008/c

LOCUS

DEFINITION

AZ960008

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0227 row: G column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0227G21"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gil4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 18 TTAGGG 13

RESULT 12

TA158A03P/c
LOCUS TA158A03P 20 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 158a03, forward sequence,
genomic survey sequence.

ACCESSION AL472050
VERSION AL472050.1 GI:11837404

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 20)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="158a03"

ORIGIN

Query Match 100.0%; Score 6; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 19 TTAGGG 14

RESULT 13

TA199G02Q/c
LOCUS TA199G02Q 20 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 199g02, reverse sequence,
genomic survey sequence.

ACCESSION AL476798

VERSION AL476798.1 GI:11843362

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 20)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="199g02"

ORIGIN

Query Match 100.0%; Score 6; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
|||||
Db 20 TTAGGG 15

RESULT 14

AW248826/c
LOCUS AW248826 21 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821056.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2821056 3',
mRNA sequence.

ACCESSION AW248826

VERSION AW248826.1 GI:6591819

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 21)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2821056.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DPD cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 21 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
 Plate: L1CM5 row: N column: 1
 High quality sequence stop: 21.
 Location/Qualifiers
 1. .21
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821056"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Query Match 100.0%; Score 6; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
 |||||
 Db 20 TTAGGG 15

RESULT 15
 AW248836/c
 LOCUS
 DEFINITION 2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3', mRNA linear EST 07-JAN-2000
 mRNA sequence.
 ACCESSION AW248836
 VERSION
 KEYWORDS
 EST. GI:6591829
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 21)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2821108.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DPD cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 10 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
 Plate: L1CM5 row: P column: 5
 High quality sequence stop: 10.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821108"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source

Location/Qualifiers

1. .21

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2821108"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 7"

/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 6; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
 |||||
 Db 20 TTAGGG 15

Search completed: August 11, 2004, 18:58:54
 Job time : 723.925 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:38:14 ; Search time 1269.68 Seconds
(without alignments)
682.741 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20
Sequence: 1 gcatgcattacattacgacg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_nam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	20	100.0	20	6	AX268760	AX268760 Sequence
C 2	14.8	74.0	120	6	E08557	E08557 Synthetic D
C 3	14.8	74.0	120	6	E08556	E08556 Synthetic D
C 4	14.2	71.0	153	6	BD246071	BD246071 Developme
C 5	14.2	71.0	166	11	AF025868	AF025868 Aegilops
C 6	14.2	71.0	178	1	BA1RRDA01	W79375 Bacterium A
C 7	13.8	69.0	162	6	AR355576	AX355576 Sequence
C 8	13.8	69.0	196	6	AX909486	AX909486 Sequence
C 9	13.8	69.0	196	6	BD045019	BD045019 Sequence
C 10	13.6	68.0	58	6	I13500	I13500 Sequence 34
C 11	13.6	68.0	58	6	I13501	I13501 Sequence 35
C 12	13.6	68.0	76	6	E08558	E08558 Synthetic D
C 13	13.6	68.0	76	6	E08558	E08558 Synthetic D
C 14	13.6	68.0	76	6	E08557	E08557 Synthetic D
C 15	13.6	68.0	76	6	E08567	E08567 Synthetic D
C 16	13.6	68.0	135	11	AU049687	AU049687 Rattus o
C 17	13.4	67.0	28	6	E06768	E06768 Synthetic o
C 18	13.4	67.0	28	6	I12026	I12026 Sequence 10
C 19	13.4	67.0	42	6	AR032363	AR032363 Sequence
C 20	13.4	67.0	42	6	I30220	I30220 Sequence 6
C 21	13.4	67.0	70	6	AR032364	AR032364 Sequence
C 22	13.4	67.0	70	6	AR032365	AR032365 Sequence
C 23	13.4	67.0	70	6	I30221	I30221 Sequence 7
C 24	13.4	67.0	70	6	I30222	I30222 Sequence 8
C 25	13.4	67.0	124	6	E08556	E08556 Synthetic D
C 26	13.4	67.0	124	6	E08565	E08565 Synthetic D
C 27	13.2	66.0	33	6	AR285607	AR285607 Sequence
C 28	13.2	66.0	33	6	AX297790	AX297790 Sequence
C 29	13.2	66.0	97	11	AU025275	AU025275 Rattus no
C 30	13.2	66.0	117	4	SHPMAF36P	M80519 Ovis aries
C 31	13.2	66.0	134	8	AX594611	AX594611 Arabidops
C 32	13.2	66.0	152	6	AX912126	AX912126 Sequence
C 33	13.2	66.0	152	6	BD047659	BD047659 Sequence
C 34	13.2	66.0	177	6	AR244933	AR244933 Sequence
C 35	13.2	66.0	187	11	G03687	G03687 human STS W
C 36	13.2	66.0	194	11	BX546013	BX546013 Arabidops
C 37	13	65.0	17	6	AX194495	AX194495 Sequence
C 38	13	65.0	17	6	AX465445	AX465445 Sequence
C 39	13	65.0	33	6	AX684461	AX684461 Sequence
C 40	13	65.0	133	9	HUMPODAT07	D17705 Homo sapien
C 41	13	65.0	150	6	AX196369	AX196369 Sequence
C 42	13	65.0	150	6	AX196371	AX196371 Sequence
C 43	13	65.0	180	8	CNS01D6K	AX116436 Botrytis
C 44	12.8	64.0	91	10	MMSCFT3	AF083887 Mus muscu
C 45	12.8	64.0	102	11	BX663678	BX663678 Arabidops

ALIGNMENTS

RESULT 1
AX268760
LOCUS AX268760 20 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 8 from Patent WO0174342.
ACCESSION AX268760
VERSION AX268760.1 GI:16541832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 8 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

```

FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA Fragment"
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 8.9;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTACG 20
    |||||
DB 1 GCATGCATGCATTACGTACG 20
    |||||

RESULT 2
E08557/c
LOCUS      120 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probes and primers.
ACCESSION E08557
VERSION   E08557.1 GI:2176672
KEYWORDS  JP 1994343498-A/3.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 120)
AUTHORS   Kato, K. and Kuriyama, A.
TITLE     NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
JOURNAL   Patent: JP 1994343498-A 3 20-DEC-1994;
          CANON INC
COMMENT   OS None
          OC Artificial sequences.
          PN JP 1994343498-A/3
          PD 20-DEC-1994
          PF 03-JUN-1993 JP 1993133640
          PI KATO KINYA, KURIYAMA AKIRA
          PC C12Q1/68;
          CC strandedness: Single;
          CC topology: Linear;
          FH Key
          FT Location/Qualifiers
          FT source 1..120
          FT /organism='Artificial sequences'.

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        /mol_type="genomic DNA"
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  Best Local Similarity 88.9%; Pred. No. 5.7e+03;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTA 18
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DB 24 GCATGCATGCATTATATA 7
    |||||

RESULT 4
BD246071/c
LOCUS      153 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD246071
VERSION   BD246071.1 GI:33055841
KEYWORDS  JP 2002531107-A/806.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 153)
AUTHORS   Pelletier, J., Gros, P. and Dubow, M.
TITLE     Development of novel antibiotics based on bacteriophage genomics
JOURNAL   Patent: JP 2002531107-A 806 24-SEP-2002;
          PHAGETECH INC
COMMENT   OS Staphylococcus aureus bacteriophage 44AHJD
          PN JP 2002531107-A/806
          PD 24-SEP-2002
          PF 03-DEC-1999 JP 2000585456
          PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
          28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
          01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 PI JERRY
          PELLETIER, PHILLIPPE GROS, MICHAEL DUBOW
          PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
          PC C12M1/00,
          PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
          C12N15/00,
          PC A61K37/02
          CC Coding Sequences
          FH Key
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          FT source 1..153
          FT /organism='Staphylococcus
          aureus bacteriophage 44AHJD'.

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ORIGIN

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Query Match      71.0%; Score 14.2; DB 6; Length 153;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCGTACGATTACGTAC 19
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Db 70 GCATACGTCGATTCGTTTC 52

RESULT 5
AF025868          166 bp DNA linear STS 12-JAN-2001
LOCUS             Aegilops markgrafii RAPD marker generated by Operon primer OP003,
DEFINITION        sequence tagged site.
ACCESSION         AF025868
VERSION           AF025868.1 GI:4090919
KEYWORDS           STS.
SOURCE            Aegilops markgrafii
ORGANISM           Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Pooideae; Triticeae; Aegilops.
REFERENCE         Sun, L.-H. and Wang, R.-C.
AUTHORS           Identification and sequences of RAPD markers for Aegilops caudata
TITLE            chromosomes
JOURNAL           Unpublished
REFERENCE         2 (bases 1 to 166)
AUTHORS           Sun, L.-H. and Wang, R.-C.
TITLE            Direct Submission
JOURNAL           Submitted (20-SEP-1997) FRRL, USDA-ARS, 695 N 1100 E, Logan, UT
                  84322-6300, USA
FEATURES           Location/Qualifiers
                   1..166
                    /organism="Aegilops markgrafii"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:4494"
                    /chromosome="F; G"
                    /note="RAPD marker generated by Operon primer OP003; C
                    genome; in the two addition lines derived from the
                    amphiploid of Triticum aestivum X Aegilops caudata"
primer_bind       1..10
                  /PCR_conditions="25 ul reaction mix containing 1X buffer,
                  3 mM MgCl2, 2 units of AmpliTaq DNA polymerase Stoffel
                  fragment (Perkin Elmer), 0.24 mM dNTP, 100 ng primer, and
                  40 ng template DNA. Amplification was accomplished with 40
                  cycles of 1 min at 94 C, 1 min at 36 C, and 2 min at 72 C
                  using the fastest transitions available"
primer_bind       complement(156..166)

ORIGIN
Query Match      71.0%; Score 14.2; DB 11; Length 166;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCGTACGATTACGTACG 20
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Db 48 CATGCAAGATTACTTACG 66

RESULT 6
BAIRDA01/c        178 bp rRNA linear BCT 26-JAN-1996
LOCUS             Bacterium ALV 16S rRNA sequence.
DEFINITION        M79375
ACCESSION         M79375.1 GI:173814
KEYWORDS           16S ribosomal RNA.
SEGMENT           1 of 3
SOURCE            bacterium ALV
ORGANISM           Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae.
REFERENCE         Lane, D.J., Harrison, A.P. Jr., Stahl, D., Pace, B., Giovannoni, S.J.,
AUTHORS           complement(156..166)

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Olsen, G.J. and Pace, N.R.
Evolutionary relationships among sulfur- and iron-oxidizing
subacteria
J. Bacteriol. 174 (1), 269-278 (1992)
MEDLINE 92104973
PUBMED 1729214
COMMENT Original source text: Bacterium ALV (individual isolate ALV) rRNA.
FEATURES           Location/Qualifiers
                   1..178
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                    /db_xref="taxon:31975"
                   1..178
                    /gene="16S rRNA"
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ORIGIN
Query Match      71.0%; Score 14.2; DB 1; Length 178;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCGTACGATTACGTACG 20
    ||||| ||||| ||||| |||||
Db 60 CTTGCAATGATTACGCACG 42

RESULT 7
AR355576          162 bp DNA linear PAT 17-AUG-2003
LOCUS             Sequence 1694 from patent US 6593114.
DEFINITION        AR355576
ACCESSION         AR355576
VERSION           AR355576.1 GI:33761660
KEYWORDS           .
SOURCE            Unknown.
ORGANISM           Unclassified.
REFERENCE         1 (bases 1 to 162)
AUTHORS           Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
                  Rosen, C.A.
TITLE            Staphylococcus aureus polynucleotides and sequences
JOURNAL           Patent: US 6593114-A 1694 15-JUL-2003;
FEATURES           Location/Qualifiers
                   1..162
                    /organism="unknown"
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ORIGIN
Query Match      69.0%; Score 13.8; DB 6; Length 162;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCATGCGTACGTTACG 20
    ||||| ||||| ||||| |||||
Db 50 TACATGCAATACGTACG 66

RESULT 8
AX909486/c        196 bp DNA linear PAT 18-DEC-2003
LOCUS             Sequence 25349 from Patent EPI033401.
DEFINITION        AX909486
ACCESSION         AX909486
VERSION           AX909486.1 GI:40065566
KEYWORDS           .
SOURCE            Homo sapiens (human)
ORGANISM           Homo sapiens
                  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
AUTHORS           Expressed sequence tags and encoded human proteins
TITLE            Patent: EP 1033401-A 25349 06-SEP-2000;
JOURNAL           Genset (FR)

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FEATURES
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  Best Local Similarity 88.2%; Pred. No. 1.9e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 3 ATGCATGCATTACGTAC 19
      ||||| ||| |||
  Db 31 ATGCATGCTTTATGTAC 15

RESULT 9
BD045019/c
LOCUS BD045019 196 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD045019
VERSION BD045019.1 GI:22586761
KEYWORDS JP 2001269182-A/21265.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 196)
  Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
  Sequence tag and encoded human protein
  Patent: JP 2001269182-A 21265 02-OCT-2001;
  GENSET
  OS Homo sapiens (human)
  PN JP 2001269182-A/21265
  PD 02-OCT-2001
  PF 24-FEB-2000 JP 2000118773
  PR 26-FEB-1999 US 60/122487
  PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
  PI JORDAN
  PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
  C12N5/10.
  PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
  CC G06F15/40
  FH Key
  Location/Qualifiers.
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ORIGIN
  Query Match      69.0%; Score 13.8; DB 6; Length 196;
  Best Local Similarity 88.2%; Pred. No. 1.9e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 3 ATGCATGCATTACGTAC 19
      ||||| ||| |||
  Db 31 ATGCATGCTTTATGTAC 15

RESULT 10
I13500
LOCUS I13500 58 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 34 from patent US 5436391.
ACCESSION I13500
VERSION I13500.1 GI:910841
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 58)
  Fujimoto, H., Ito, K., Yamamoto, M. and Shimamoto, K.
  NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
  Patent: JP 1994343498-A 4 20-DEC-1994;
  CANON INC
  OS None
  NC Artificial sequences.
  PN JP 1994343498-A/4
  PD 20-DEC-1994
  PF 03-JUN-1993 JP 1993133640
  PI KATO KINYA, KURIYAMA AKIRA
  PC C12Q1/68;
  CC strandedness: Single;
  CC topology: Linear;
  FH Key
  Location/Qualifiers

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TITLE Synthetic insecticidal gene, plants of the genus oryza transformed
  with the gene, and production thereof
JOURNAL Patent: US 5436391-A 34 25-JUL-1995;
FEATURES
  source
    Location/Qualifiers
      1..58
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ORIGIN
  Query Match      68.0%; Score 13.6; DB 6; Length 58;
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  Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 1 GCATGCATGCATTACGTACG 20
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  Db 9 GCATGCATGAATTCCTAGG 28

RESULT 11
I13501/c
LOCUS I13501 58 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 35 from patent US 5436391.
ACCESSION I13501
VERSION I13501.1 GI:910842
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 58)
  Fujimoto, H., Ito, K., Yamamoto, M. and Shimamoto, K.
  Synthetic insecticidal gene, plants of the genus oryza transformed
  with the gene, and production thereof
  Patent: US 5436391-A 35 25-JUL-1995;
  Location/Qualifiers
  source
    Location/Qualifiers
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ORIGIN
  Query Match      68.0%; Score 13.6; DB 6; Length 58;
  Best Local Similarity 80.0%; Pred. No. 2.7e+04;
  Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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  Db 54 GCATGCATGAATTCCTAGG 35

RESULT 12
E08558
LOCUS E08558 76 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for probes and primers.
ACCESSION E08558
VERSION E08558.1 GI:2176673
KEYWORDS JP 1994343498-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
  1 (bases 1 to 76)
  Kato, K. and Kuriyama, A.
  NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
  Patent: JP 1994343498-A 4 20-DEC-1994;
  CANON INC
  OS None
  NC Artificial sequences.
  PN JP 1994343498-A/4
  PD 20-DEC-1994
  PF 03-JUN-1993 JP 1993133640
  PI KATO KINYA, KURIYAMA AKIRA
  PC C12Q1/68;
  CC strandedness: Single;
  CC topology: Linear;
  FH Key
  Location/Qualifiers

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FT Location/Qualifiers
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Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
||||| |||
Db 53 GCATGCATGCATCGCGCG 72

RESULT 13
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LOCUS 76 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for probes and primers.
ACCESSION E08558
VERSION E08558.1 GI:2176673
KEYWORDS JP 1994343498-A/4.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 76)
Kato,K. and Kuriyama,A.
NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
TITLE Patent: JP 1994343498-A 4 20-DEC-1994;
JOURNAL CANON INC

COMMENT
OS None
OC Artificial sequences.
PN JP 1994343498-A/4
PD 20-DEC-1994
PF 03-JUN-1993 JP 1993133640
PI KATO KINYA, KURIYAMA AKIRA
PC C12Q1/68;
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CC topology: Linear;
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
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Db 26 GCATGCATGCATCGCTCG 7

RESULT 14
E08567/c
LOCUS 76 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe and primer.
ACCESSION E08567
VERSION E08567.1 GI:2176682
KEYWORDS JP 1994343499-A/5.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 76)
Kato,K.
METHOD FOR DETECTING NUCLEIC ACID
TITLE Patent: JP 1994343499-A 5 20-DEC-1994;
JOURNAL CANON INC
COMMENT
OS None
OC Artificial sequences.
PN JP 1994343499-A/5
PD 20-DEC-1994
PF 04-JUN-1993 JP 1993134615
PI KATO KINYA
PC C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
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FT Location/Qualifiers
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Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
||||| |||
Db 53 GCATGCATGCATCGCGCG 72

RESULT 15
E08567/c
LOCUS 76 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe and primer.
ACCESSION E08567
VERSION E08567.1 GI:2176682
KEYWORDS JP 1994343499-A/5.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 76)
Kato,K.
METHOD FOR DETECTING NUCLEIC ACID
TITLE Patent: JP 1994343499-A 5 20-DEC-1994;
JOURNAL CANON INC
COMMENT
OS None
OC Artificial sequences.
PN JP 1994343499-A/5
PD 20-DEC-1994
PF 04-JUN-1993 JP 1993134615
PI KATO KINYA
PC C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
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FT Location/Qualifiers
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ORIGIN
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Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
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Db 26 GCATGCATGCATCACGCTCG 7
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OM nucleic - nucleic search, using sw model

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Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacattacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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8: geneseqn2003bs.*
9: geneseqn2003cs.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	20	2	Aaz10697 Oligonucl
2	20	100.0	20	4	Aas14912 Melanogen
3	20	100.0	20	8	ACD25827 Melanogen
4	20	100.0	20	8	ACD25777 Oligonucl
5	15.2	76.0	42	6	ABK91410 Multiple
6	15.2	76.0	42	6	ABK91409 Multiple
7	14.8	74.0	120	2	AAQ95093 Configura
8	14.8	74.0	120	2	AAQ84038 Plasmid p
9	14.2	71.0	141	7	ACA23973 Prokaryot
10	14.2	71.0	153	3	AAAG9048 Bacterioph
11	13.8	69.0	162	2	AAV76005 Staphyloc
12	13.8	69.0	196	3	AACT21274 Human sec
13	13.6	68.0	28	2	AAT29051 Maltogen
14	13.6	68.0	76	2	AAQ95094 Configura
15	13.6	68.0	76	2	AAQ95094 Configura
16	13.6	68.0	76	2	AAQ84039 Plasmid p
17	13.6	68.0	76	2	AAQ84039 Plasmid p
18	13.4	67.0	70	2	AAQ35972 Oligonucl
19	13.4	67.0	124	2	AAQ95092 Configura
20	13.4	67.0	124	2	AAQ84037 Plasmid p
21	13.4	67.0	175	7	ABX91312 Murine ge
22	13.2	66.0	33	5	AAAD19373 Rhipopus
23	13.2	66.0	152	3	AAC23914 Human sec

C 24	13.2	66.0	177	7	ABX81832 Corn ear-
C 25	13	65.0	17	4	AAC80675 Immunogen
C 26	13	65.0	17	4	AAS09645 Immunorea
C 27	13	65.0	17	6	ABK46523 Immunosti
C 28	13	65.0	33	7	AAD48011 BGMV DNAB
C 29	13	65.0	130	6	ABL75969 Corn tass
C 30	13	65.0	150	5	AAI61445 Soybean 2
C 31	13	65.0	150	5	AAI61447 Soybean 2
C 32	12.8	64.0	37	7	ABZ69169 E coli is
C 33	12.8	64.0	40	2	AAT34008 Primer fo
C 34	12.8	64.0	60	6	ABN37518 Human spl
C 35	12.8	64.0	99	2	AAQ34156 Downstrea
C 36	12.8	64.0	138	3	AAC59405 Human sec
C 37	12.8	64.0	182	3	AAC08211 Human sec
C 38	12.8	64.0	195	7	ACF56778 Rice endo
C 39	12.6	63.0	26	2	AAQ46972 Helper Pr
C 40	12.6	63.0	27	3	AAA15194 PCR prime
C 41	12.6	63.0	32	3	AAA37803 Helicobac
C 42	12.6	63.0	33	6	ABA04987 Human tel
C 43	12.6	63.0	41	6	ABV76426 Ribosomal
C 44	12.6	63.0	59	9	ADB39029 Sample DN
C 45	12.6	63.0	65	3	AAA14518 PCR prime

ALIGNMENTS

RESULT 1
AAZ10697
ID AAZ10697 standard; DNA; 20 BP.
XX
AC AAZ10697;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
FN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-00006758.
XX
PR 26-MAR-1998; 98US-00048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases.
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are UV mimetics and protect
CC cells against subsequent exposure to UV-irradiation or chemicals. The
CC oligonucleotides are useful for increasing p53 activity in a cell,
CC reducing the susceptibility to UV-induced hyperproliferative diseases,
CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,
CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and
XX reducing susceptibility to skin cancer
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
DB 1 GCATGCATGCATTACGTACG 20
|||||

RESULT 2
ID AAS14912 standard; DNA; 20 BP.
XX AAS14912;
DT 14-FEB-2002 (first entry)
XX Melanogenesis associated oligonucleotide #8.
DE
XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= g
FT /note= "Phosphorylated"
XX
XX WO200174342-A2.
XX
PD 11-OCT-2001.
XX
XX
PF 30-MAR-2001; 2001WO-US010162.
XX
XX 31-MAR-2000; 2000US-00540843.
XX
XX (UYBO-) UNIV BOSTON.
PA
XX Gilchrest BA, Yaar M, Eller M;
PI
XX WPI; 2001-626338/72.
XX
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
PT carcinoma, using specific oligonucleotides that mimic the effects of
PT ultra-violet light.
XX
XX Claim 1; Page 39; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell
XX proliferation by treating cells with at least one oligonucleotide, or its
XX fragment. The compounds, which have cytostatic, anti-allergic, anti-
XX inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX DNA repair processes (or a protective response to later exposure to
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
XX or a tumour necrosis factor inhibitor. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX pathway, resulting in transient arrest of cell growth, allowing more time
XX for DNA repair to occur before cell division takes place. The method is
XX especially used to treat carcinoma but may also be used to: treat other
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
XX allergically mediated inflammation (atopic or contact dermatitis,
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
XX cells caused by radiation or chemicals; increase melanin production
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to

CC promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
CC sequence is melanogenesis associated oligonucleotide #8, a synthetic
CC peptide that resembles the fragment excised during excision repair of
CC thymine dimers and one of the oligonucleotides used to inhibit mammalian
CC epithelial cell proliferation, described in the method of the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
DB 1 GCATGCATGCATTACGTACG 20
|||||

RESULT 3
ID ACD25827 standard; DNA; 20 BP.
XX ACD25827;
AC ACD25827;
DT 08-SEP-2003 (first entry)
XX
XX Melanogenic telomere-like oligonucleotide #2.
DE
XX
KW Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological;
KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;
KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;
KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;
KW gp-1100; hyperproliferative disorder; spongiosis; blistering;
KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;
KW actinic keratosis; Bowen's disease; basal cell carcinoma; liver cancer;
KW atopic dermatitis; breast cancer; lung cancer; prostate cancer;
KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;
KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;
KW stomach cancer; thyroid cancer.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "5' phosphorylated"
XX
XX US2003032610-A1.
XX
PD 13-FEB-2003.
XX
XX 12-APR-2002; 2002US-00122630.
XX
XX 03-JUN-1996; 96WO-US008386.
PR 26-MAR-1998; 98US-00048927.
PR 31-MAR-2000; 2000US-00540843.
PR 30-MAR-2001; 2001WO-US010162.
XX
XX (GILC/) GILCHREST B A.
PA (ELLE/) ELLER M S.
PA (YAAR/) YAAR M.
XX
XX Gilchrest BA, Eller MS, Yaar M;
XX WPI; 2003-512221/48.
XX
XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,
PT by administering composition having oligonucleotides that share sequence
PT identity with human telomere overhang repeat.
XX
XX Claim 44; Page 18; 65pp; English.

XX The invention relates to inhibiting growth of cancer cells, which is
 CC independent of presence or activity of telomerase in cells, not requiring
 CC the presence or activity of p53 normal function in cells, or resulting in
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,
 CC involving administering a composition comprising oligonucleotides which
 CC share at least 50% sequence identity with human telomere overhang repeat,
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their
 CC contiguous portion) and is used in a method inhibiting proliferation of
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging
 CC chemicals. The method is useful for inhibiting growth of cancer cells
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in
 CC human, promoting differentiation of malignant cells in a mammal,
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer
 CC cells (especially melanoma cells) in a human and for treatment of other
 CC hyperproliferative disorders (e.g. spongiolysis, blistering or dyskeratosis
 CC in the skin of a mammal, skin cancer in a human with xeroderma
 CC pigmentosum, seboreic keratosis, actinic keratosis, Bowen's disease, or
 CC basal cell carcinoma) and for treating or preventing pre-cancerous
 CC conditions affecting epithelial cells (such as psoriasis and atopic
 CC dermatitis) and also the types of cancers of breast, lung, liver,
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,
 CC oesophagus, stomach, and thyroid. The present sequence is a melanogenic
 CC telomere-like oligonucleotide of the invention
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCATGCATGCATTACGTACG 20
 Db 1 GCATGCATGCATTACGTACG 20
 RESULT 4
 ACD25777
 ID ACD25777 standard; DNA; 20 BP.
 AC ACD25777;
 XX
 XX 28-AUG-2003 (first entry)
 DE
 DE Oligonucleotide with homology to telomere pTPT sequence.
 KW ss, human telomere overhang repeat; proliferative disease; cytostatic;
 KW antiproliferative; dermatological; cancer; apoptosis; skin cancer;
 KW UV irradiation-induced skin; oxidative damage; lymphoma; osteosarcoma;
 KW melanoma; leukaemia; cervical cancer; squamous cell carcinoma;
 KW spongiolysis; blistering; dyskeratosis; xeroderma pigmentosum;
 KW seboreic keratosis; actinic keratosis; Bowen's disease;
 KW basal cell carcinoma; pre-cancerous condition; epithelial cell;
 KW psoriasis; atopic dermatitis.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT modified_base 1
 FT /tag= a
 FT /mod base= OTHER
 FT /note= "5, phosphorylated"
 XX
 PN US2003032611-A1.
 XX
 PD 13-FEB-2003.
 XX
 XX 12-APR-2002; 2002US-00122633.
 XX
 XX 31-MAR-2000; 2000US-00540843.
 PR

PR 30-MAR-2001; 2001WO-US010162.
 XX (GILC/) GILCHREST B A.
 PA (ELLE/) ELLER M S.
 PA (YAAR/) YAAR M.
 XX
 XX Gilchrest BA, Eller MS, Yaar M;
 PI WPT; 2003-512222/48.
 DR
 DR
 PT Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,
 PT by administering composition having oligonucleotides that share sequence
 PT identity with human telomere overhang repeat.
 XX
 PS Claim 44; Page 18; 64pp; English.
 CC The invention relates to inhibiting growth of cancer cells (which is
 CC independent of the presence or activity of telomerase in cells) not
 CC requiring the presence or activity of p53 normal function in cells, or
 CC resulting in S-phase arrest in cells, and inducing apoptosis in the
 CC cancer cells, comprising administering a composition comprising
 CC oligonucleotides which share at least 50% sequence identity with human
 CC telomere overhang repeat (TTAGG)n. The method also involves promoting
 CC differentiation of malignant cells in a mammal, enhancing the expression
 CC of one or more surface antigens indicative of differentiation of cancer
 CC cells in a human, by administering the oligonucleotide. The
 CC oligonucleotide is further administered to enhance repair of UV
 CC irradiation-induced damage to the skin in a human, reduce oxidative
 CC damage in a mammal and to reduce proliferation of keratinocytes in the
 CC skin of a human. The composition comprises oligonucleotides such as
 CC pGAGTATGAG, pCATAC, pGTAGGTTAG, pGGTATGAGTT, pTAGATGCGTG, and a
 CC physiological carrier. Oligonucleotides such as pTAGAGGAT, pAGTATGA,
 CC pGTATG, pCCCTAA, pAGTATGA and pGCATGCATGCATTACGTACG may be administered
 CC along with those detailed above. The method is useful for inhibiting
 CC growth of cancer cells, especially lymphoma, osteosarcoma, melanoma,
 CC leukaemia, cervical cancer, squamous cell carcinoma, in a human. The
 CC method is also useful for inducing apoptosis in cancer cells in human,
 CC promoting differentiation of malignant cells in a mammal and enhancing
 CC the expression of one or more surface antigens (e.g. MART-1, tyrosinase,
 CC TRP-1 or gp-1100) indicative of differentiation of cancer cells,
 CC especially melanoma cells, for inhibiting proliferation of epithelial
 CC cells, for preventing or reducing DNA damage in epithelial cells in a
 CC mammal, where the cells are epithelial cells. The composition is
 CC preferably useful for treating a hyperproliferative disorder in human. A
 CC composition comprising pGAGTATGAG and pTPT, is useful for preventing
 CC spongiolysis, blistering or dyskeratosis in the skin of a mammal, following
 CC exposure to UV light, reducing the occurrence of skin cancer in a human
 CC with xeroderma pigmentosum or for enhancing repair of UV irradiation-
 CC induced damage to skin in a human, treating melanoma and reducing
 CC proliferation of keratinocytes in the skin, where the human has
 CC seboreic keratosis, actinic keratosis, Bowen's disease, squamous cell
 CC carcinoma or basal cell carcinoma. The method is useful for treating or
 CC preventing pre-cancerous conditions affecting epithelial cells such as
 CC psoriasis and atopic dermatitis, and also the types of cancers of breast,
 CC lung, liver, prostate, pancreatic, ovarian, bladder, uterine, colon,
 CC brain, oesophagus, stomach, and thyroid. The present sequence is a
 CC oligonucleotide with homology to the telomere pTPT sequence shown to
 CC increase pigmentation in melanoma cells
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCATGCATGCATTACGTACG 20
 Db 1 GCATGCATGCATTACGTACG 20
 RESULT 5
 ABK91410
 ID ABK91410 standard; DNA; 42 BP.

```

XX AC ABK91410;
XX DT 05-NOV-2002 (first entry)
XX DE Multiple cloning site for retroviral vectors #2.
XX ds; long terminal repeat; LTR; gag; cytotstatic; multiple cloning site;
KW envelope protein; retroviral vector; cancer; virally-induced disease;
KW virucide; gene therapy.
XX OS Synthetic.
XX WO200260490-A1.
XX PN 08-AUG-2002.
XX PD 31-JAN-2002; 2002WO-US002632.
XX PF 31-JAN-2001; 2001US-0265123P.
XX PR (UYDU-) UNIV DUKE.
XX PA Smith CA, Gilboa E;
XX PI WPI; 2002-619210/66.
XX DR A new Moloney Murine Leukemia Virus-based retroviral vector, designated
XX PT as LUV, useful for expressing a retroviral cell for treating genetic
XX PT disorders, or diseases induced by pathogens such as cancer or virally-
XX PT induced disease.
XX PS Example 1; Page 13; 50pp; English.
XX CC The invention relates to a retroviral vector comprising 5' to 3' and in
CC operable linkage, a 5' long terminal repeat (LTR), a splice donor, a
CC packaging sequence, a gag open reading frame (ORF) mutated to reduce
CC translation of gag peptides, a splice acceptor, a start codon in frame
CC with a DNA sequence and a 3' LTR. Also included are producing an
CC infectious viral particle comprising transfecting the retroviral vector
CC into a retroviral packaging cell line under conditions to produce the
CC viral particle, and recovering the viral particle, a packaging cell
CC comprising the retroviral vector, introducing a transcription unit into a
CC eukaryotic cell comprising infecting the cell with the viral particle and
CC a pharmaceutical composition comprising the retroviral vector, a
CC packaging cell comprising the retroviral vector or the viral particle or
CC a eukaryotic cell infected by the viral particle, and a carrier, diluent,
CC adjuvant or excipient. The vector is useful in expressing a retroviral
CC cell for treating genetic disorders or diseases induced by pathogens such
CC as cancer or virally induced disease. The methods are useful for
CC preparing the retroviral vector. The vector provides high titre,
CC efficient expression of foreign genes, and safety. The present sequence
CC is a multiple cloning site suitable for inclusion in the vectors of the
CC invention
XX SQ Sequence 42 BP; 8 A; 13 C; 15 G; 6 T; 0 U; 0 Other;
XX Query Match 76.0%; Score 15.2; DB 6; Length 42;
XX Best Local Similarity 85.0%; Pred. No. 3.8e-02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTAGCTAGC 20
DB 23 GCGTGCATGCATGCCGTAGC 42
RESULT 6
ABK91409/c
ID ABK91409 standard; DNA; 42 BP.
XX AC ABK91409;
XX DT 05-NOV-2002 (first entry)

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XX DE Multiple cloning site for retroviral vectors #1.
XX ds; long terminal repeat; LTR; gag; cytotstatic; multiple cloning site;
KW envelope protein; retroviral vector; cancer; virally-induced disease;
KW virucide; gene therapy.
XX OS Synthetic.
XX WO200260490-A1.
XX PN 08-AUG-2002.
XX PD 31-JAN-2002; 2002WO-US002632.
XX PF 31-JAN-2001; 2001US-0265123P.
XX PR (UYDU-) UNIV DUKE.
XX PA Smith CA, Gilboa E;
XX PI WPI; 2002-619210/66.
XX DR A new Moloney Murine Leukemia Virus-based retroviral vector, designated
XX PT as LUV, useful for expressing a retroviral cell for treating genetic
XX PT disorders, or diseases induced by pathogens such as cancer or virally-
XX PT induced disease.
XX PS Example 1; Page 13; 50pp; English.
XX CC The invention relates to a retroviral vector comprising 5' to 3' and in
CC operable linkage, a 5' long terminal repeat (LTR), a splice donor, a
CC packaging sequence, a gag open reading frame (ORF) mutated to reduce
CC translation of gag peptides, a splice acceptor, a start codon in frame
CC with a DNA sequence and a 3' LTR. Also included are producing an
CC infectious viral particle comprising transfecting the retroviral vector
CC into a retroviral packaging cell line under conditions to produce the
CC viral particle, and recovering the viral particle, a packaging cell
CC comprising the retroviral vector, introducing a transcription unit into a
CC eukaryotic cell comprising infecting the cell with the viral particle and
CC a pharmaceutical composition comprising the retroviral vector, a
CC packaging cell comprising the retroviral vector or the viral particle or
CC a eukaryotic cell infected by the viral particle, and a carrier, diluent,
CC adjuvant or excipient. The vector is useful in expressing a retroviral
CC cell for treating genetic disorders or diseases induced by pathogens such
CC as cancer or virally induced disease. The methods are useful for
CC preparing the retroviral vector. The vector provides high titre,
CC efficient expression of foreign genes, and safety. The present sequence
CC is a multiple cloning site suitable for inclusion in the vectors of the
CC invention
XX SQ Sequence 42 BP; 6 A; 15 C; 13 G; 8 T; 0 U; 0 Other;
XX Query Match 76.0%; Score 15.2; DB 6; Length 42;
XX Best Local Similarity 85.0%; Pred. No. 3.8e-02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTAGCTAGC 20
DB 24 GCGTGCATGCATGCCGTAGC 5
RESULT 7
AAQ95093/c
ID AAQ95093 standard; DNA; 120 BP.
XX AC AAQ95093;
XX DT 02-OCT-1995 (first entry)
XX DE Configuration detecting nucleic acid probe #3.
XX KW Probe; PCR; terminus; amplify; primer; configuration; ss.

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XX OS Synthetic.
XX FH Key
XX FH primer_bind
XX FT Location/Qualifiers
XX FT 1. .12
XX FT /*tag= a
XX FT /note= "PCR primer binding site"
XX FT 109. .120
XX FT /*tag= b
XX FT /note= "PCR primer binding site"
XX FT
XX PN JP06343498-A.
XX XX
XX PD 20-DEC-1994.
XX XX
XX XX 03-JUN-1993; 93JP-00133640.
XX XX
XX PR 03-JUN-1993; 93JP-00133640.
XX XX
XX PA (CANO ) CANON KK.
XX XX
XX DR WPI; 1995-069322/10.
XX XX
XX PT Nucleic acid probe - and method for detecting nucleic acid.
XX PS Example 1; Col 4; 6pp; Japanese.
XX XX
XX CC Probes (AAQ95091-4) can be used in a method for the detection of a
XX CC nucleic acid target sequence which has PCR-controlled termini and can be
XX CC amplified by PCR. The probes can be used to detect configuration
XX XX
XX SQ Sequence 120 BP; 30 A; 30 C; 30 G; 30 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 2; Length 120;
Best Local Similarity 88.9%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTA 18
Db 24 GCATGCATGCATTATATA 7

RESULT 9
ACA23973/c
ID ACA23973 standard; DNA; 141 BP.
XX AC
XX AC ACA23973;
XX DT
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #5630.
XX KW
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX OS
XX OS Borrelia cepacia.
XX PN
XX PN WO200277183-A2.
XX XX
XX XX 03-OCT-2002.
XX XX
XX PF 21-MAR-2002; 2002WO-US009107.
XX XX
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA
XX PA (ELIT-) ELITRA PHARM INC.
XX PI
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX XX
XX DR WPI; 2003-029926/02.
XX DR P-PSDB; ABU20103.
XX XX
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX XX
XX PS Claim 14; SEQ ID NO 11843; 1766pp; English.
XX XX
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

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CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation or screening for homologous nucleic acids required
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX
 SQ Sequence 141 BP; 28 A; 41 C; 51 G; 21 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 7; Length 141;
 Best Local Similarity 84.2%; Pred. NO. 1.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
 |||||
 Db 38 GCCTGCATGCATTACGGAC 20
 |||||

RESULT 10
 AAA69048/C
 ID AAA69048 standard; DNA; 153 BP.
 XX
 AC AAA69048;
 XX

DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX

DE Bacteriophage 44AHJD nucleotide sequence 44HJDORF031.

XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 XX

OS Staphylococcus phage 44AHJD.

XX WO200032825-A2.

XX 08-JUN-2000.

XX 03-DEC-1999; 99WO-IB002040.

XX 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00454252.

XX (PHAG-) PHAGETECH INC.

XX Pelletier J, Gros P, Dubow M;

XX WPI; 2000-412361/35.

XX P-PSDB; AAB16563.

XX Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

XX Example 9; Page 278; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAA69243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX

SQ Sequence 153 BP; 52 A; 21 C; 27 G; 53 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 153;
 Best Local Similarity 84.2%; Pred. NO. 1.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
 |||||
 Db 70 GCATACCTGCATTACGTTTC 52
 |||||

RESULT 11
 AAV76005
 ID AAV76005 standard; DNA; 162 BP.

XX AC AAV76005;

XX DT 16-MAR-1999 (first entry)

XX Staphylococcus aureus contig SEQ ID #1694.

XX Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.

XX Staphylococcus aureus.

XX EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.

XX Claim 1; Page 2035; 3271pp; English.

XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the *S. aureus* DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against *S. aureus* infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the *S. aureus* DNA sequences contained on the computer
 CC readable medium

XX

SQ Sequence 162 BP; 46 A; 28 C; 33 G; 54 T; 0 U; 1 Other;
 Query Match 69.0%; Score 13.8; DB 2; Length 162;
 Best Local Similarity 88.2%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 TGCATGCATTACGTACG 20
 DB 50 TACATGCAATACGTACG 66
 AAC21274/c
 ID AAC21274 standard; cDNA; 196 BP.
 XX
 AC AAC21274;
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 25349.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 DR WPI; 2000-500381/45.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors
 XX
 SQ Sequence 196 BP; 68 A; 35 C; 34 G; 58 T; 0 U; 1 Other;
 Query Match 69.0%; Score 13.8; DB 3; Length 196;
 Best Local Similarity 88.2%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 ATGCATGCATTACGTAC 19
 DB 31 ATGCATGCTTTATGTAC 15
 RESULT 13
 AAT29051
 ID AAT29051 standard; DNA; 28 BP.
 XX
 AC AAT29051;
 XX
 DT 03-OCT-1996 (first entry)
 XX
 DE Maltogenic alpha-amylase signal peptide PCR primer DK16.
 XX
 KW Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis;
 KW lytic enzyme; beta-glucan degradation; cell wall lysis; pigment;
 KW colorant; flavour; yeast extract; protoplast; Oerskovia xanthineolytica;
 KW polymerase chain reaction; primer; PCR; alpha-amylase; signal peptide;
 KW Bacillus stearothermophilus; ss.
 XX
 OS Synthetic.
 XX
 PN WO9612013-A1.
 XX
 PD 25-APR-1996.
 XX
 PF 16-OCT-1995; 95WO-DK000414.
 XX
 PR 14-OCT-1994; 94DK-00001192.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Ferrer P, Diers I, Hedegaard L, Halkier T, Asenjo JA, Savva D;
 DR WPI; 1996-222000/22.
 XX
 CC DNA construct encoding enzyme with beta-1,3-glucanase activity - useful
 CC for modifying or degrading beta-glucan contg. material and in the prepn.
 CC of e.g. food colourants, flavourings and yeast extracts.
 XX
 PS Example 7; Page 22; 60pp; English.
 XX
 CC Primers DK15 (AAT29050) and DK16 (AAT29051) were used for the PCR
 CC amplification of the ribosome binding site and signal peptide coding
 CC regions of the Bacillus stearothermophilus maltogenic alpha-amylase gene
 CC in pBN520. The PCR product was used to construct pPPF1, which also
 CC carried a gene (AAT29043) for Oerskovia xanthineolytica beta-1,3-
 CC glucanase (AAR97362). Transformation of Bacillus subtilis strain DN1885
 CC or protease-deficient strain Toc46 allowed prodn. of the Oerskovia lytic
 CC enzyme
 XX
 SQ Sequence 28 BP; 10 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 68.0%; Score 13.6; DB 2; Length 28;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GCATGCATGCATTACGTACG 20
 DB 4 GCAAGCTTGCAATTACGAAG 23
 RESULT 14
 AAQ95094
 ID AAQ95094 standard; DNA; 76 BP.
 XX
 AC AAQ95094;
 XX
 DT 02-OCT-1995 (first entry)
 XX
 DE Configuration detecting nucleic acid probe #4.
 XX
 KW Probe; PCR; terminus; amplify; primer; configuration; ss.
 XX
 OS Synthetic.
 XX
 FH Key primer_bind 65..76
 FT Location/Qualifiers

```
FT FT /*tag= a
XX /note= "PCR primer binding site"
PN JP06343498-A.
XX
XX 20-DEC-1994.
PD
XX 03-JUN-1993; 93JP-00133640.
XX
XX 03-JUN-1993; 93JP-00133640.
XX
XX (CANO ) CANON KK.
XX
XX WPI; 1995-069322/10.
XX
XX Nucleic acid probe - and method for detecting nucleic acid.
XX
XX Example 1; Col 4; 6pp; Japanese.
XX
CC Probes (AAQ95091-4) can be used in a method for the detection of a
CC nucleic acid target sequence which has PCR-controlled termini and can be
CC amplified by PCR. The probes can be used to detect configuration
XX
SQ Sequence 76 BP; 18 A; 22 C; 23 G; 13 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 2; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTACG 20
Db 53 GCATGCATGCATCGCGCG 72
RESULT 15
AAQ95094/c
ID AAQ95094 standard; DNA; 76 BP.
XX
XX AC AAQ95094;
XX
XX 02-OCT-1995 (first entry)
XX
XX Configuration detecting nucleic acid probe #4.
XX
XX Probe; PCR; terminus; amplify; primer; configuration; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT primer_bind 65..76
FT FT /*tag= a
FT FT /note= "PCR primer binding site"
XX
XX JP06343498-A.
XX
XX 20-DEC-1994.
XX
XX 03-JUN-1993; 93JP-00133640.
XX
XX 03-JUN-1993; 93JP-00133640.
XX
XX (CANO ) CANON KK.
XX
XX WPI; 1995-069322/10.
XX
XX Nucleic acid probe - and method for detecting nucleic acid.
XX
XX Example 1; Col 4; 6pp; Japanese.
XX
CC Probes (AAQ95091-4) can be used in a method for the detection of a
CC nucleic acid target sequence which has PCR-controlled termini and can be
CC amplified by PCR. The probes can be used to detect configuration
XX
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```
SQ Sequence 76 BP; 18 A; 22 C; 23 G; 13 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 2; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTACG 20
Db 26 GCATGCATGCATCGCGCTCG 7
Search completed: August 11, 2004, 17:56:35
Job time : 292.366 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 16:50:49 ; Search time 2394.19 Seconds
(without alignments)
249.455 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20
Sequence: 1 gcatgcattacacgacg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estm.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	85.0	110	28	AQ965378 LERIB78TR
2	15.8	79.0	127	14	CD725785 312 Penni
3	15.8	79.0	136	10	AW581082 RCI-LT005
4	15.8	79.0	142	10	AW935636 QV3-DT001

5	15.8	79.0	177	28	BZ411188
6	15.4	77.0	177	28	CC440642
7	15.4	77.0	199	10	BE833189
8	15.4	77.0	200	10	BB737705
9	15.2	76.0	137	28	CC434123
10	15.2	76.0	155	14	CF078438
11	15.2	76.0	165	28	BH866954
12	15.2	76.0	166	12	BJ250639
13	15.2	76.0	171	28	BH619747
14	15.2	76.0	182	29	CG408774
15	15.2	76.0	183	12	BM370416
16	15	75.0	109	12	BG266669
17	14.8	74.0	42	28	AZ771346
18	14.8	74.0	109	13	BQ613131
19	14.8	74.0	145	28	AZ114630
20	14.8	74.0	151	9	AW101085
21	14.8	74.0	154	10	BE939102
22	14.8	74.0	156	29	CG306670
23	14.8	74.0	162	10	BE058631
24	14.8	74.0	168	28	BH317050
25	14.8	74.0	178	28	BH870273
26	14.8	74.0	180	10	AW678292
27	14.8	74.0	191	14	CA820487
28	14.8	74.0	192	29	AG262468
29	14.4	72.0	119	12	B1119966
30	14.4	72.0	123	9	AI920345
31	14.2	71.0	92	28	B43951
32	14.2	71.0	103	14	W66964
33	14.2	71.0	116	13	BQ589121
34	14.2	71.0	119	12	BP014192
35	14.2	71.0	120	28	BZ586324
36	14.2	71.0	135	28	CC021359
37	14.2	71.0	135	29	CG935001
38	14.2	71.0	147	28	BZ419418
39	14.2	71.0	154	13	BX608931
40	14.2	71.0	156	9	AA129771
41	14.2	71.0	163	12	BG362444
42	14.2	71.0	167	10	BE076919
43	14.2	71.0	168	13	BW287445
44	14.2	71.0	170	10	AW787508
45	14.2	71.0	170	12	BG155382

ALIGNMENTS

RESULT 1
AQ965378
LOCUS LERIB78TR LERG Arabidopsis thaliana genomic clone LERIB78, genomic
DEFINITION survey sequence.
ACCESSION AQ965378
VERSION AQ965378.1 GI:6793079
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 110)
Buell,C.R.; Lin,X.; Pai,G.; Barnstead,M.; Bowman,C.; Utterbach,T.,
Feldblyum,T.; Liang,F.; Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For additional information, see <http://www.tigr.org/tdb/at/at.html>

Seq primer: TR
Class: shotgun.

FEATURES
source
1..110
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="LANDSBERG ERRECTA"
/db_xref="taxon:3702"
/clone="LERIB78"
/clone_lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."

ORIGIN

Query Match 85.0%; Score 17; DB 28; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17
|||||
Db 31 GCATGCATGCATTACGT 47

RESULT 2

CD725785
LOCUS 127 bp mRNA linear EST 26-JUN-2003
DEFINITION 312 Pennisetum glaucum seedlings exposed to salt (500 mM NaCl)
ACCESSION Pennisetum glaucum cDNA clone 312, mRNA sequence.
CD725785
VERSION CD725785.1 GI:32276632
KEYWORDS EST.
SOURCE Pennisetum glaucum
ORGANISM Pennisetum glaucum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Paniceae; Pennisetum.
1 (bases 1 to 127)
Mishra,R.N., Markandeya,G., Nair,S., Reddy,A.R., Sopory,S.K. and Reddy,M.K.

REFERENCE

AUTHORS
TITLE Analysis of Expressed Sequence Tags from a subtracted cDNA library prepared from Pennisetum glaucum seedlings that were exposed to salt (500 mM NaCl) stress
JOURNAL Unpublished (2003)
COMMENT Contact: Reddy MK
Plant Molecular Biology Laboratory
International Centre for Genetic Engineering and Biotechnology (ICGEB)

Aruna Asaf Ali Marg, New Delhi 110067, INDIA
Tel: 91-11-26181242
Fax: 91-11-26162316
Email: redy@icgeb.res.in.

FEATURES

source
1..127
Location/Qualifiers
/organism="Pennisetum glaucum"
/mol_type="mRNA"
/db_xref="taxon:4543"
/clone="312"
/tissue_type="Entire leaf tissue"
/dev_stage="Two-week-old seedlings"
/clone_lib="Pennisetum glaucum seedlings exposed to salt (500 mM NaCl)"
/note="Organ: Leaf; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 79.0%; Score 15.8; DB 14; Length 127;
Best Local Similarity 89.5%; Pred. No. 5.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
|||||

Db 46 GCAAGCATGCATTACGCAC 64
|||||

RESULT 3

AW581082
LOCUS 136 bp mRNA linear EST 16-MAR-2000
DEFINITION RC1-LT0056-070100-011-all LT0056 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW581082
VERSION AW581082.1 GI:7256131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 136)

REFERENCE

HCGP <http://www.ludwig.org.br/ORESTES>.

AUTHORS

The FAPESP/LICR Human Cancer Genome Project

JOURNAL

Unpublished (1999)

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-27049322
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-LT0056-070100-011-all&t3=2000-01-07&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 136.

FEATURES

source

1..136
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="LT0056"
/note="Organ: leiomyos; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 79.0%; Score 15.8; DB 10; Length 136;
Best Local Similarity 89.5%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
|||||

Db 8 CATGCAGGCATTACCTACG 26
|||||

RESULT 4

AW935636
LOCUS 142 bp mRNA linear EST 30-MAY-2000
DEFINITION QV3-DT0012-081299-021-f04 DT0012 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW935636
VERSION AW935636.1 GI:8111042
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,P.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.O., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=QV3-DF0012-081>)
299-021-f04&t3=199-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 55
High quality sequence stop: 142.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="DF0012"

/note="Organ: denis drash; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 79.0%; Score 15.9; DB 10; Length 142;
Best Local Similarity 89.5%; Pred. No. 5.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
|||||
Db 25 GCAGCGATGCACCTACGTAC 7

RESULT 5

BZ411188
LOCUS CGACT10TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0031B20,
DEFINITION genomic survey sequence.
ACCESSION BZ411188
VERSION BZ411188.1 GI:26044395
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Bases 1 to 177)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

Location/Qualifiers
1. .177
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0031B20"
/clone_lib="ZM_0.7_1.5_KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 79.0%; Score 15.8; DB 28; Length 177;
Best Local Similarity 89.5%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
|||||

Db 69 CATGCATGCCTACGTACG 87
|||||

RESULT 6

CC440642
LOCUS PUHGV17TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTA448C10,
DEFINITION genomic survey sequence.
ACCESSION CC440642
VERSION CC440642.1 GI:30941919
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Bases 1 to 177)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUHGV17D
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

Location/Qualifiers
1. .177
/organism="Zea mays"
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/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA448C10"
/clone_lib="ZM_0.6_1.0_KB"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN

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Best Local Similarity 94.1%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19
|||||

Db 34 AGGCATGCATTACGTAC 50
|||||

RESULT 7

BE833189
LOCUS BE833189 199 bp mRNA linear EST 22-SEP-2000

```

DEFINITION QV3-OT0063-120700-263-h06 OT0063 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE833189
VERSION BE833189.1 GI:10265567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=6t2=QV3-OT0063-120
700-263-h06&t3=2000-07-12&t4=1)
Seg primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 199.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="OT0063"
/note="Organ: ovary; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
ORIGIN
Query Match 77.0%; Score 15.4; DB 10; Length 199;
Best Local Similarity 94.1%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTA 18
|||||
Db 164 CATTTCATGCATTACGTA 180

RESULT 8
BB737705/c
LOCUS BB737705
DEFINITION BB737705 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F430015B13 3', mRNA sequence.
ACCESSION BB737705
VERSION BB737705.1 GI:16136855
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 200)

```

AUTHORS

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Mateuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,K., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL

Unpublished (2001)

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Kira,A. Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.

FEATURES

Location/Qualifiers
1..200
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F430015B13"
/tissue_type="spleen"
/dev_stage="6 days neonate"
/clone_lib="RIKEN full-length enriched, 6 days neonate spleen"

ORIGIN

Query Match 77.0%; Score 15.4; DB 10; Length 200;
Best Local Similarity 94.1%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTA 18

|||||

Db 93 CATGCATGCATAACGTA 77

RESULT 9

CC434123/c

LOCUS CC434123

DEFINITION CC434123

genomic survey sequence.

ACCESSION CC434123

VERSION CC434123.1

KEYWORDS GSS

SOURCE Zea mays

ORGANISM Zea mays

CC434123
F0004343TB 0.6_1.0 KB Zea mays genomic clone ZMMBTa62H14,
137 bp DNA linear GSS 20-MAY-2003

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 137)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J.

TITLE

Maize Genomics Consortium

JOURNAL

Unpublished (2003)

COMMENT

Other_GSSs: PUHJB43TD

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cgtg.org

Seq primer: TR

Class: sheared ends.

FEATURES

source
1..137
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMB7a462H14"
/clone_lib="ZM 0.6-1.0 KB"
/note="vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Query Match 76.0%; Score 15.2; DB 28; Length 137;
Best Local Similarity 85.0%; Pred. No. 9.6e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20

|||||
Db 70 GCATGCATGCATTACTACG 51

RESULT 10

CF078438

LOCUS

DEFINITION
QHK2H04.YG.ab1 OH K sunflower H.paradoxus Helianthus paradoxus cDNA
clone QHK2H04, mRNA sequence.

ACCESSION

CF078438

VERSION

CF078438.1 GI:33117481

KEYWORDS

EST.

SOURCE

ORGANISM

Helianthus paradoxus

Helianthus paradoxus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Asteroidae;

Heliantheae; Helianthus.

1 (bases 1 to 155)

REFERENCE

AUTHORS

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,

Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,

Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,

Lai,Z., Church,S., Jackson,L. and Bradford,K.

Letuce and sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmore]

Department of Vegetable Crops, R.W.Michelmore Lab

University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@cgtg.org [michelmore@vegmail.ucdavis.edu]

Singleton, see http://cgpdb.ucdavis.edu/ for details.

Plate: QHK2 row: H column: 04.

Seq primer: QHK2

Class: Location/Qualifiers

1..155

/organism="Helianthus paradoxus"

/mol_type="mRNA"

/db_xref="taxon:73304"

/clone="QHK2H04"

/lab_host="E.coli"

/clone_lib="OH K sunflower H.paradoxus"

/notes="Vector: pERCNDSFIAB; The library was constructed

from four different sources (seedling, root, leaf and

flower) of RNA from a single genotype. cDNAs were pooled

and directionally cloned into a custom medium-copy vector.

Details of library construction can be obtained at

http://cgpdb.ucdavis.edu/"

ORIGIN

Query Match 76.0%; Score 15.2; DB 14; Length 155;
Best Local Similarity 85.0%; Pred. No. 9.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20

|||||
Db 102 GCATGCATGCATCGCTAAG 121

RESULT 11

BH866954

LOCUS

DEFINITION

hg92c06.y8 WGS-ZmaysF (JMI07 adapted methyl filtered) Zea mays

genomic clone hg92c06 5', genomic survey sequence.

ACCESSION

BH866954

VERSION

BH866954.1 GI:22102851

KEYWORDS

GSS.

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 165)

REFERENCE

AUTHORS

Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N.,

Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,

Zutavern,T., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hg92 row: c column: 06

Seq primer: -21M13UnivRev

Class: shotgun

High quality sequence stop: 165.

FEATURES

source

1..165

Location/Qualifiers

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="hg92c06"

/lab_host="JMI07 or DH5a"

/clone_lib="WGS-ZmaysF (JMI07 adapted methyl filtered)"

/notes="Organ: Immature ears; Site 1: Xba I; Site 2: Xba I;

The vector was digested with XbaI and one nucleotide was

added by fill in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size

fractionated using sephadex. The resulting fragments were

between 0.8 and 3 kb and were cloned into the vector

(.x/y reads in M13mp19, .b/g reads in pUC19). The same

ligation was transformed in either JM107 or DH5a."

ORIGIN

Query Match 76.0%; Score 15.2; DB 28; Length 165;

Best Local Similarity 85.0%; Pred. No. 1e+04;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
 ||||| ||||| ||||| |||||
 Db 141 GCATGCACGCTGACGTACG 160

RESULT 12
 BJ250639/c 166 bp mRNA linear EST 05-APR-2002
 LOCUS BJ250639 Y. Ogihara unpublished cDNA library, Wh_f Triticum
 DEFINITION aestivum cDNA clone whf16104 3', mRNA sequence.
 ACCESSION BJ250639
 VERSION BJ250639.1 GI:20060605
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.
 1 (bases 1 to 166)
 Ogihara, Y. and Murai, K.
 Expressed genes in Triticum aestivum
 Unpublished (2002)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1..166
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="whf16104"
 /tissue_type="spike at flowering date"
 /dev_stage="Feekes' scale 10.5.1"
 /clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"

FEATURES

source
 Query Match 76.0%; Score 15.2; DB 12; Length 166;
 Best Local Similarity 85.0%; Pred. No. 1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GCATGCATGCATTACGTACG 20
 ||||| ||||| ||||| |||||
 Db 131 GCATGCATGATTGCGTGG 112

ORIGIN

Query Match 76.0%; Score 15.2; DB 12; Length 166;
 Best Local Similarity 85.0%; Pred. No. 1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
 ||||| ||||| ||||| |||||
 Db 131 GCATGCATGATTGCGTGG 112

RESULT 13
 BH619747 171 bp DNA linear GSS 30-JAN-2002
 LOCUS 1007063C12.2EL y1 1007 - RescueMu Grid H Zea mays genomic, genomic
 DEFINITION survey sequence.

ACCESSION BH619747
 VERSION BH619747.1 GI:18430811
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 171)
 Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon
 Unpublished (2001)
 TITLE Unpublished (2001)
 JOURNAL
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1007062 column: 18
 Class: transposon-tagged.
 Location/Qualifiers
 1..171
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"

FEATURES

source
 Query Match 76.0%; Score 15.2; DB 28; Length 171;
 Best Local Similarity 85.0%; Pred. No. 1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GCATGCATGCATTACGTACG 20
 ||||| ||||| ||||| |||||
 Db 40 GCATGCATGCATCAGCAATG 59

ORIGIN

Query Match 76.0%; Score 15.2; DB 28; Length 171;
 Best Local Similarity 85.0%; Pred. No. 1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
 ||||| ||||| ||||| |||||
 Db 40 GCATGCATGCATCAGCAATG 59

RESULT 14

CG408774/c 182 bp DNA linear GSS 03-SEP-2003
 LOCUS Ds467 Ds insertion lines Oryza sativa (japonica cultivar-group)
 DEFINITION genomic, genomic survey sequence.

ACCESSION CG408774
 VERSION CG408774.1 GI:34430139
 KEYWORDS GSS.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 182)
 Kim, C.M., Piao, H.L., Park, S.J., Chon, N.S., Je, B.I., Sun, B.,
 Park, S.H., Park, J.Y., Lee, E.J., Kim, M.J., Lee, J.J., Nam, M.H.,
 Eun, M.Y. and Han, C.D.

Rapid, large-scale generation of Ds transposant lines and analysis
 of Ds loci in rice
 Unpublished (2003)
 Contact: Chang-deok Han
 Division of Applied Life Science, PMBRC
 Gyeongsang National University
 Gajwa-dong 900, Jinju 660-701, South Korea
 Tel: +82 55 751 6029
 Fax: +82 55 759 9363
 Email: cdhan@nongae.gsnu.ac.kr
 Location: chromosome 3 clone OSJNBb0011G21
 Class: transposon-tagged.
 Location/Qualifiers
 1..182
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"

FEATURES

source

Job time : 2400.86 secs

/cultivar="Dongjin"
/db_xref="taxon:39947"
/clone_lib="Ds insertion lines"

ORIGIN

Query Match 76.0%; Score 15.2; DB 29; Length 182;
Best Local Similarity 85.0%; Pred. No. 1e+04; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 118 GCATGCATGCATGCACACG 99

RESULT 15

BM370416 183 bp mRNA linear EST 23-JUL-2002
EBro08_SQ004_C17_R root, 3 week, drought-stressed, cv Optic, EBro08
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBro08_SQ004_C17 5', mRNA
sequence.
ACCESSION BM370416
VERSION BM370416.1 GI:18113806
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 183)
AUTHORS Hedley,P., Liu,H., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.

FEATURES

source
1..183 Location/Qualifiers
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBro08_SQ004_C17"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, drought-stressed, cv Optic,
EBro08"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old drought stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEERAD funded cereal IGF (Investigating
Gene Function) project."

ORIGIN

Query Match 76.0%; Score 15.2; DB 12; Length 183;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 116 GCATTCATGTACTACGTACG 135

Search completed: August 11, 2004, 18:58:49

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:57:26 ; Search time 60 Seconds
(without alignments)
184.984 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcatgattacgtaag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	69.0	162	4	US-08-956-171E-1694
2	13.6	68.0	58	1	US-07-982-712-34
3	13.6	68.0	58	1	US-07-982-712-35
4	13.4	67.0	28	1	US-08-053-564-10
5	13.4	67.0	42	1	US-08-301-872A-6
6	13.4	67.0	42	2	US-08-443-372A-6
7	13.4	67.0	70	1	US-08-301-872A-7
8	13.4	67.0	70	1	US-08-301-872A-8
9	13.4	67.0	70	2	US-08-443-372A-7
10	13.4	67.0	70	2	US-08-443-372A-8
11	13.2	66.0	33	4	US-09-535-851A-6
12	13.2	66.0	177	4	US-09-313-294A-292
13	12.6	63.0	26	1	US-07-720-586-7
14	12.6	63.0	65	3	US-09-415-522-24
15	12.6	63.0	108	4	US-08-956-171E-4834
16	12.6	63.0	129	4	US-08-956-171E-4790
17	12.6	63.0	178	4	US-09-313-294A-26
18	12.4	62.0	38	2	US-09-097-759-6
19	12.4	62.0	38	3	US-09-065-104-24
20	12.4	62.0	59	2	US-08-816-155B-23
21	12.4	62.0	59	3	US-08-815-809-8
22	12.4	62.0	59	3	US-09-079-587-23
23	12.4	62.0	138	1	US-08-500-234-5
24	12.4	62.0	138	1	US-08-386-921-5
25	12.4	62.0	141	1	US-08-386-921-13
26	12.4	62.0	144	1	US-08-386-921-11
27	12.4	62.0	147	1	US-08-386-921-9

C 28	12.4	62.0	161	1	US-08-600-234-2	Sequence 2, Appli
C 29	12.4	62.0	161	1	US-08-386-921-2	Sequence 2, Appli
C 30	12.4	62.0	161	1	US-08-386-921-10	Sequence 10, Appli
C 31	12.4	62.0	197	1	US-08-386-921-4	Sequence 4, Appli
C 32	12.2	61.0	20	4	US-08-234-312B-21	Sequence 21, Appli
C 33	12.2	61.0	20	4	US-08-468-024B-21	Sequence 21, Appli
C 34	12.2	61.0	20	4	US-08-465-679-21	Sequence 21, Appli
C 35	12.2	61.0	21	4	US-08-187-757D-19	Sequence 19, Appli
C 36	12.2	61.0	21	4	US-08-210-143C-19	Sequence 19, Appli
C 37	12.2	61.0	30	4	US-09-504-358-43	Sequence 43, Appli
C 38	12.2	61.0	30	4	US-09-954-314-43	Sequence 43, Appli
C 39	12.2	61.0	35	4	US-09-122-315C-15	Sequence 15, Appli
C 40	12.2	61.0	35	4	US-09-360-376-4	Sequence 4, Appli
C 41	12.2	61.0	39	2	US-08-452-724A-18	Sequence 18, Appli
C 42	12.2	61.0	39	4	US-08-453-623-18	Sequence 18, Appli
C 43	12.2	61.0	43	3	US-08-961-810-31	Sequence 31, Appli
C 44	12.2	61.0	43	3	US-08-352-902D-31	Sequence 31, Appli
C 45	12.2	61.0	43	4	US-09-265-503B-31	Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-08-956-171E-1694
; Sequence 1694, Application US/08956171E
; Patent No. 6593114

; GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 1694:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

US-08-956-171E-1694

Query Match 69.0%; Score 13.8; DB 4; Length 162;
Best Local Similarity 88.2%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCATGCATTACGTACG 20
Db 50 TACATGCAATACGTACG 66

RESULT 2
US-07-982-712-34
Sequence 34, Application US/07982712
Patent No. 5436391
GENERAL INFORMATION:
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH
APPLICANT: Mikihiko YAMAMOTO, and Ko SHIMAMOTO
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,712
FILING DATE: 19921127
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-07-982-712-34

Query Match 68.0%; Score 13.6; DB 1; Length 59;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
Db 9 GCATGCATGAATTCCTAGG 28

RESULT 3
US-07-982-712-35/c
Sequence 35, Application US/07982712
Patent No. 5436391
GENERAL INFORMATION:
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH
APPLICANT: Mikihiko YAMAMOTO, and Ko SHIMAMOTO
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,712
FILING DATE: 19921127
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-07-982-712-35

Query Match 68.0%; Score 13.6; DB 1; Length 58;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
Db 54 GCATGCATGAATTCCTAGG 35

RESULT 4
US-08-053-564-10/c
Sequence 10, Application US/08053564
Patent No. 5418153
GENERAL INFORMATION:
APPLICANT: MORI, MASASHI
APPLICANT: OKUNO, TETSURO
APPLICANT: FURUSAWA, IWAO
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF
TITLE OF INVENTION: EXOGENOUS GENE OR ITS PRODUCT
TITLE OF INVENTION: IN PLANT CELLS NO.2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,564
FILING DATE: 28-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI-4-152593
FILING DATE: 28-APR-1992
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 649113
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: synthesized oligonucleotide
US-08-053-564-10

Query Match 67.0%; Score 13.4; DB 1; Length 28;
Best Local Similarity 93.3%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACG 16
| | | | | | | | | | | | | | | |
Db 20 CATGCATGCATTCG 6

RESULT 5
US-08-301-872A-6
Sequence 6, Application US/08301872A
Patent No. 580734
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-301-872A-6

Query Match 67.0%; Score 13.4; DB 1; Length 42;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCATGCATTACGTAC 19
| | | | | | | | | | | | | | | |
Db 12 GGATGCATTACGTAC 26

RESULT 6
US-08-443-372A-6
Sequence 6, Application US/08443372A
Patent No. 5869239
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,372A
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/301,872
FILING DATE: 06-SEP-1994
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-443-372A-6

Query Match 67.0%; Score 13.4; DB 2; Length 42;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCATGCATTACGTAC 19
| | | | | | | | | | | | | | | |
Db 12 GGATGCATTACGTAC 26

RESULT 7
US-08-301-872A-7/c
Sequence 7, Application US/08301872A

Patent No. 5580734
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIORITY INFORMATION:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-301-872A-7

Query Match 67.0%; Score 13.4; DB 1; Length 70;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTACG 20
| | | | | | | | | |
Db 54 CATGCATTACGTAGG 40

RESULT 8
US-08-301-872A-8
Sequence 8, Application US/08301872A
Patent No. 5580734
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIORITY INFORMATION:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-301-872A-8

Query Match 67.0%; Score 13.4; DB 1; Length 70;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTACG 20
| | | | | | | | | |
Db 17 CATGCATTACGTAGG 31

RESULT 9
US-08-443-372A-7/c
Sequence 7, Application US/08443372A
Patent No. 5869239
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,372A
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/301,872
FILING DATE: 06-SEP-1994
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIORITY INFORMATION:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-443-372A-7

Query Match 67.0%; Score 13.4; DB 2; Length 70;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTAG 20
Db 54 CATGCATTACGTAG 40
|||||

RESULT 10

US-08-443-372A-8
Sequence 8, Application US/08443372A
Patent No. 5869239
GENERAL INFORMATION:

APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,372A
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/301,872
FILING DATE: 06-SEP-1994
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-443-372A-8

Query Match 67.0%; Score 13.4; DB 2; Length 70;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTAG 20
Db 17 CATGCATTACGTAG 31
|||||

RESULT 11

US-09-535-851A-6
Sequence 6, Application US/09535851A
Patent No. 6528636
GENERAL INFORMATION:
APPLICANT: Battelle Memorial Institute
TITLE OF INVENTION: A Promoter Sequence of 3-Phosphoglycerate Kinase Gene 2 of Lactic
Patent No. 6528636
TITLE OF INVENTION: Producing Fungus Rhizopus Oryzae and a Method of Expressing a Gene
FILE REFERENCE: E-1891B
CURRENT APPLICATION NUMBER: US/09/535,851A
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in version 3.1
SEQ ID NO 6
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-535-851A-6

Query Match 66.0%; Score 13.2; DB 4; Length 33;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTA 18
Db 4 GCATGCATGCATTTCATA 21
|||||

RESULT 12

US-09-313-294A-292/c
Sequence 292, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Ialguidi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 292
LENGTH: 177
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700548929H1
NAME/KEY: unsure
LOCATION: 2, 6, 75-93
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-292

Query Match 66.0%; Score 13.2; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTA 18
Db 52 GCATGCATGCATGCCATA 35
|||||

RESULT 13

US-07-720-586-7
 ; Sequence 7, Application US/07720586
 ; Patent No. 5232831
 ; GENERAL INFORMATION:
 ; APPLICANT: Curt Millman
 ; APPLICANT: Philip W. Hammond
 ; TITLE OF INVENTION: NUCLEIC ACIDS PROBES
 ; TITLE OF INVENTION: TO STREPTOCOCCUS PYOGENES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 611 West Sixth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90017
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 ; SOFTWARE: WordPerfect (Version 5.0)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/720,586
 ; FILING DATE: 19910628
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 193/121
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-07-720-586-7

Query Match 63.0%; Score 12.6; DB 1; Length 26;
 Best Local Similarity 78.9%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
 Db 3 CTTGCATGTATTAGGCACG 21

RESULT 14

US-09-415-522-24/c
 ; Sequence 24, Application US/09415522A
 ; Patent No. 6291660
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaffney, Thomas
 ; APPLICANT: Wendland, Juergen
 ; APPLICANT: Philippsen, Peter
 ; TITLE OF INVENTION: No. 6291660e1 Fungal Genes Required For No. 6291660mal Growth And
 ; TITLE OF INVENTION: Development
 ; FILE REFERENCE: CGC2046
 ; CURRENT APPLICATION NUMBER: US/09/415,522A
 ; CURRENT FILING DATE: 1999-10-08
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patentin ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 65

TYPE: DNA

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Primer
 US-09-415-522-24

Query Match 63.0%; Score 12.6; DB 3; Length 65;
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
 Db 57 GCTTGCATGCCTTTCATAC 39

RESULT 15

US-08-956-171E-4834/c
 ; Sequence 4834, Application US/08956171E
 ; Patent No. 6593114
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; APPLICANT: Gil H. Choi
 ; APPLICANT: Patrick S. Dillon
 ; APPLICANT: Craig A. Rosen
 ; APPLICANT: Steven C. Barash
 ; APPLICANT: Michael R. Fannon
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5256
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-Oct-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 4834:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4834:
 US-08-956-171E-4834

Query Match 63.0%; Score 12.6; DB 4; Length 108;
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
 Db 40 CTTGCATGTATTAGGCACG 22

Thu Aug 12 09:23:33 2004

us-09-540-843-8.szlm200.rni

Page 7

Search completed: August 11, 2004, 19:33:24
Job time : 61 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 19:00:04 ; Search time 288.387 Seconds
(without alignments)
340.279 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacacgtacg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 2263564

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	15	US-10-122-630-8
2	20	100.0	20	15	US-10-122-633-8
C 3	14.2	71.0	141	13	US-10-282-122A-11843
C 4	14.2	71.0	153	12	US-09-727-892-32
C 5	14.2	71.0	175	17	US-10-437-963-71654
C 6	14.2	71.0	191	17	US-10-437-963-32687
7	13.8	69.0	162	8	US-08-781-986A-1694
8	13.8	69.0	162	13	US-10-329-624-1694
9	13.8	69.0	173	13	US-10-424-599-76449
10	13.8	69.0	177	13	US-10-424-599-1569
C 11	13.8	69.0	180	13	US-10-424-599-59127
12	13.8	69.0	187	13	US-10-424-599-76527
13	13.6	68.0	112	17	US-10-437-963-46744
C 14	13.6	68.0	165	13	US-10-085-783A-18933

C 15	13.6	68.0	165	16	US-10-242-535A-18933
16	13.6	68.0	179	17	US-10-437-963-87658
17	13.6	68.0	187	17	US-10-021-323-16957
C 18	13.4	67.0	175	9	US-09-728-444-656
C 19	13.4	67.0	188	13	US-10-424-599-129131
C 20	13.2	66.0	99	9	US-09-969-373-431
C 21	13.2	66.0	99	9	US-09-969-373-516
C 22	13.2	66.0	128	13	US-10-424-599-65688
C 23	13.2	66.0	131	17	US-10-437-963-96687
C 24	13.2	66.0	138	16	US-10-260-238-5712
25	13.2	66.0	139	13	US-10-085-783A-6262
26	13.2	66.0	139	16	US-10-242-535A-6262
27	13.2	66.0	157	13	US-10-424-599-66570
28	13.2	66.0	188	13	US-10-424-599-32750
C 29	13	65.0	17	15	US-10-194-035-95
30	13	65.0	106	9	US-09-969-373-854
31	13	65.0	106	9	US-09-969-373-855
C 32	13	65.0	109	9	US-09-969-373-494
C 33	13	65.0	130	9	US-09-234-093B-5343
34	13	65.0	150	10	US-09-754-853A-76
35	13	65.0	150	10	US-09-754-853A-78
C 36	13	65.0	182	9	US-09-923-876-2073
C 37	13	65.0	182	11	US-09-923-876-2073
C 38	12.8	64.0	60	10	US-09-908-975-10266
39	12.8	64.0	100	9	US-09-969-373-168
C 40	12.8	64.0	111	17	US-10-437-963-20497
C 41	12.8	64.0	145	13	US-10-424-599-59525
42	12.8	64.0	149	13	US-10-424-599-62748
C 43	12.8	64.0	172	13	US-10-424-599-48011
44	12.8	64.0	190	9	US-09-969-373-169
45	12.6	63.0	50	13	US-10-147-368-4

ALIGNMENTS

RESULT 1
US-10-122-630-8
; Sequence 8, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-8

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20
|||||
Db 1 GCATGCATGCATTACGTACG 20

RESULT 2

US-10-122-633-8
; Sequence 8, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-8

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 GCATGCATGCATTACGTACG 20
|||||
Db 1 GCATGCATGCATTACGTACG 20

RESULT 3

US-10-282-122A-11843/c
; Sequence 11843, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11843
; LENGTH: 141
; TYPE: DNA
; ORGANISM: Burkholderia cepacia
US-10-282-122A-11843

Query Match 71.0%; Score 14.2; DB 13; Length 141;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
|||||
Db 38 GCCTGCATGCAATACGGAC 20

RESULT 4

US-09-727-892-32/c
; Sequence 32, Application US/09727892
; Publication No. US20040091856A1
; GENERAL INFORMATION:
; APPLICANT: Phagotech, Inc.
; APPLICANT: PELLETIER, Jerry
; APPLICANT: GROS, Philippe
; APPLICANT: DUBOW, Michael
; TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGE 44 AHJD
; FILE REFERENCE: 073406-0302
; CURRENT APPLICATION NUMBER: US/09/727,892
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Staphylococcus aureus Bacteriophage 44 AHJD
US-09-727-892-32

Query Match 71.0%; Score 14.2; DB 12; Length 153;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
|||||
Db 70 GCATACCTGCATTACGTTTC 52

RESULT 5

US-10-437-963-71654/c
; Sequence 71654, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

```
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 71654
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72107C.1
US-10-437-963-71654

Query Match          71.0%; Score 14.2; DB 17; Length 175;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 CATGCATGCATTACGTACG 20
    |||||
Db   46 CATCCATGCATTCCTTACG 28
    |||||

RESULT 6
US-10-437-963-32687/c
; Sequence 32687, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 32687
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36871C.1
US-10-437-963-32687

Query Match          71.0%; Score 14.2; DB 17; Length 191;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 CATGCATGCATTACGTACG 20
    |||||
Db   62 CATCCATGCATTCCTGTACG 44
    |||||

RESULT 7
US-08-781-986A-1694
; Sequence 1694, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:

Query Match          71.0%; Score 14.2; DB 17; Length 191;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 CATGCATGCATTACGTACG 20
    |||||
Db   62 CATCCATGCATTCCTGTACG 44
    |||||

RESULT 8
US-10-329-624-1694
; Sequence 1694, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Gil H. Choi
; APPLICANT: Patrick S. Dillon
; APPLICANT: Craig A. Rosen
; APPLICANT: Steven C. Barash
; APPLICANT: Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:

Query Match          69.0%; Score 13.8; DB 8; Length 162;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4 TGCATGCATTACGTACG 20
    |||||
Db   50 TACATGCATACGTACG 66
    |||||

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1694:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-1694
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; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 1694:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1694:
US-10-329-624-1694

Query Match 69.0%; Score 13.8; DB 13; Length 162;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCATGCATTACGTACG 20
DB 50 TACATGCATTACGTACG 66

RESULT 9
US-10-424-599-76449
; Sequence 76449, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 76449
; LENGTH: 173
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40045C.1
US-10-424-599-76449

Query Match 69.0%; Score 13.8; DB 13; Length 173;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19
DB 48 ATGCATGCATTACAGAC 64

RESULT 10
US-10-424-599-1569
; Sequence 1569, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1569
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Glycine max

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101416C.1
US-10-424-599-1569

Query Match 69.0%; Score 13.8; DB 13; Length 177;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19
DB 98 ATGCATCCATTACTTAC 114

RESULT 11
US-10-424-599-59127/c
; Sequence 59127, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 59127
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24402C.1
US-10-424-599-59127

Query Match 69.0%; Score 13.8; DB 13; Length 180;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17
DB 178 GCATCCATGCATTGCGT 162

RESULT 12
US-10-424-599-76527
; Sequence 76527, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 76527
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(187)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40115C.1
US-10-424-599-76527

Query Match 69.0%; Score 13.8; DB 13; Length 187;

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Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCATGCATTACGTACG 20
Db 90 TGCATGCATTGCCTACG 106

RESULT 13
US-10-437-963-46744
; Sequence 46744, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 46744
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_49581C.1
US-10-437-963-46744

Query Match 68.0%; Score 13.6; DB 17; Length 112;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
Db 1 GCAAGCAACATTACGTAAAG 20

RESULT 14
US-10-085-783A-18933/c
; Sequence 18933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: Liew, C.C.
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18933
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-18933

Query Match 68.0%; Score 13.6; DB 13; Length 165;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 GCATGCATGCATTACGTACG 20
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RESULT 15
US-10-242-535A-18933/c
; Sequence 18933, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18933
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-18933

Query Match 68.0%; Score 13.6; DB 16; Length 165;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
682.741 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2199298

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Listing first 45 summaries

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21: em_or.*

22: em_ov.*

23: em_pat.*

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28: em_un.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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C 2	5	100.0	5	6	AX268758	AX268758 Sequence
C 3	5	100.0	7	6	AX268755	AX268755 Sequence
C 4	5	100.0	7	6	AX268759	AX268759 Sequence
C 5	5	100.0	8	6	AX047565	AX047565 Sequence
C 6	5	100.0	8	6	AX104946	AX104946 Sequence
C 7	5	100.0	8	6	AX119567	AX119567 Sequence
C 8	5	100.0	8	6	BD085298	BD085298 DNA-based
C 9	5	100.0	8	6	BD191357	BD191357 DNA-based
C 10	5	100.0	9	6	AX268753	AX268753 Sequence
C 11	5	100.0	9	6	AX667174	AX667174 Sequence
C 12	5	100.0	9	6	AX668771	AX668771 Sequence
C 13	5	100.0	9	6	AX668807	AX668807 Sequence
C 14	5	100.0	9	6	AX805897	AX805897 Sequence
C 15	5	100.0	9	9	S50583	S50583 type I proc
C 16	5	100.0	9	9	S50585	S50585 type I proc
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C 23	5	100.0	10	6	AR107344	AR107344 Sequence
C 24	5	100.0	10	6	AR123039	AR123039 Sequence
C 25	5	100.0	10	6	AR136787	AR136787 Sequence
C 26	5	100.0	10	6	AR160130	AR160130 Sequence
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C 28	5	100.0	10	6	BD238895	BD238895 Preparati
C 29	5	100.0	10	6	BD239131	BD239131 Preparati
C 30	5	100.0	10	6	BD239305	BD239305 Preparati
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C 34	5	100.0	10	6	BD239605	BD239605 Preparati
C 35	5	100.0	10	6	BD239634	BD239634 Preparati
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C 38	5	100.0	10	6	BD239837	BD239837 Preparati
C 39	5	100.0	10	6	BD240005	BD240005 Preparati
C 40	5	100.0	10	6	BD240133	BD240133 Preparati
C 41	5	100.0	10	6	BD240148	BD240148 Preparati
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C 43	5	100.0	10	6	BD240280	BD240280 Preparati
C 44	5	100.0	10	6	BD240281	BD240281 Preparati
C 45	5	100.0	10	6	BD240306	BD240306 Preparati

ALIGNMENTS

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LOCUS AX268756
DEFINITION Sequence 4 from Patent WO0174342.
ACCESSION AX268756
VERSION AX268756.1 GI:16541828
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Gilchrist, B.A., Yaar, M. and Eller, M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 4 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

AX268756 5 bp DNA linear PAT 29-OCT-2001
Sequence 4 from Patent WO0174342.

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RESULT 2
AX268758 AX268758 5 bp DNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 6 from Patent WO0174342.
ACCESSION AX268758
VERSION AX268758.1 GI:16541830
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 6 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
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DEFINITION Sequence 3 from Patent WO0174342.
ACCESSION AX268755
VERSION AX268755.1 GI:16541827
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 3 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
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LOCUS
DEFINITION Sequence 7 from Patent WO0174342.
ACCESSION AX268759
VERSION AX268759.1 GI:16541831
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 7 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
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Db 6 CATAC 2

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AX047565 AX047565 8 bp DNA linear PAT 15-DEC-2000
LOCUS
DEFINITION Sequence 6 from Patent WO0068399.
ACCESSION AX047565
VERSION AX047565.1 GI:11876656
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 8)
AUTHORS McIvor,R.S., Hackett,P.B. and Aguilar-Cordova,E.
TITLE Vector-mediated delivery of integrating transposon sequences
JOURNAL Patent: WO 0068399-A 6 16-NOV-2000;
REGENTS OF THE UNIVERSITY OF MINNESOTA (US); BAYLOR COLLEGE OF
MEDICINE (US); McIvor, R. Scott (US); Hackett, Perry B. (US);
Aguilar-Cordova, Estuardo (US)
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RESULT 6
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LOCUS      AX104946      8 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 1138 from Patent WO0122972.
ACCESSION  AX104946
VERSION     AX104946.1  GI:13921143
KEYWORDS    .
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE       Immunostimulatory nucleic acids
JOURNAL     Patent: WO 0122972-A 1138 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
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Db 7 CATAAC 3

RESULT 7
AX119567/c
LOCUS      AX119567      8 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 224 from Patent WO0129251.
ACCESSION  AX119567
VERSION     AX119567.1  GI:14036486
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Messiaen,L. and Callens,T.
TITLE       Improved mutation analysis of the nfi gene
JOURNAL     Patent: WO 0129251-A 224 26-APR-2001;
            UNIVERSITEIT GENT (BE)
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAAC 5
Db 7 CATAAC 3

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LOCUS      BD085298      8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION DNA-based transposon system for the introduction of nucleic acid
            into DNA of a cell.
ACCESSION  BD085298
VERSION     BD085298.1  GI:22630908
KEYWORDS    JP 2001523450-A/10.

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SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Hackett,P.B., Clark,K.J., Daple,A.J., Ekar,S.C., Larjespayda,D.A.,
            Ibycus,Z. and Issufark,T.
TITLE       DNA-based transposon system for the introduction of nucleic acid
            into DNA of a cell
JOURNAL     Patent: JP 2001523450-A 10 27-NOV-2001;
            REGENTS OF THE UNIVERSITY OF MINNESOTA
COMMENT     OS Artificial Sequence
            PN JP 2001523450-A/10
            PD 27-NOV-2001
            PF 13-NOV-1998 JP 2000521183
            PI 13-NOV-1997 US 60/065303
            P1 PERRY B HACKETT,KARL J CLARK,ADAM J DAPIE,STEVEN C EKAR, PI
            DAVID A LARJESPAYDA,ZOLTAN IVCUS,TSSUSANNA ISSUFARK PC
            C12N15/09,A01K67/027,C07K16/18,C12N5/10,C12Q1/68,C12N15/00, PC
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAAC 5
Db 2 CATAAC 6

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LOCUS      BD191357      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION DNA-based transposon system for the introduction of nucleic acid
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ACCESSION  BD191357
VERSION     BD191357.1  GI:33001096
KEYWORDS    JP 2002511741-A/10.
SOURCE      unidentified
            unidentified
            ORGANISM
            unclassified.
            1 (bases 1 to 8)
REFERENCE   1 (bases 1 to 8)
AUTHORS     Hackett,P.B., Ivics,Z., Izsvak,Z. and Caldovic,L.
TITLE       DNA-based transposon system for the introduction of nucleic acid
            into DNA of a cell
JOURNAL     Patent: JP 2002511741-A 10 16-APR-2002;
            REGENTS OF THE UNIV OF MINNESOTA
COMMENT     PN JP 2002511741-A/10
            PD 16-APR-2002
            PF 11-MAR-1998 JP 1998539720
            PI PERRY B HACKETT,ZOLTAN IVCIS,ZSUZSANNA IZSVAK,LJUBICA CALDOVIC
            PC C12N15/90,C12N5/16,A01K67/027,C07K16/18
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DEFINITION Sequence 1 from Patent WO0174342.
ACCESSION AX268753
VERSION AX268753.1 GI:16541825
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 1 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 7 CATAC 3

RESULT 11
LOCUS AX667174
DEFINITION Sequence 623 from Patent WO0242459.
ACCESSION AX667174
VERSION AX667174.1 GI:29291326
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 623 30-MAY-2002;
Sangamo Biosciences Inc. (US)
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Db 2 CATAC 6

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DEFINITION Sequence 2220 from Patent WO0242459.
ACCESSION AX668771
VERSION AX668771.1 GI:29291746
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
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JOURNAL Patent: WO 0242459-A 2220 30-MAY-2002;
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Db 8 CATAC 4

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DEFINITION Sequence 2256 from Patent WO0242459.
ACCESSION AX668807
VERSION AX668807.1 GI:29291782
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
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JOURNAL Patent: WO 0242459-A 2256 30-MAY-2002;
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ACCESSION AX805897
VERSION AX805897.1 GI:38522808
KEYWORDS
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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     van Eijk,M.J. and van Schaik,C.
TITLE       Discrimination and detection of target nucleotide sequences using
            mass spectrometry
JOURNAL     Patent: WO 03060163-A 43 24-JUL-2003;
            Keygene N.V. (NL)
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Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |||||
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DEFINITION type I procollagen [human, mRNA Mutant, 9 nt].
ACCESSION  S50583
VERSION    S50583.1 GI:233928
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
TITLE     Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
            type I procollagen in lethal osteogenesis imperfecta. The
            conformational strain on the triple helix introduced by a glycine
            substitution can be transmitted along the helix
JOURNAL   J. Biol. Chem. 266 (24), 15608-15613 (1991)
MEDLINE   91340689
PUBMED    1874719
REMARK    GenBank staff at the National Library of Medicine created this
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Query Match      100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.8e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 15:32:08 ; Search time 72.2581 Seconds
(without alignments)
293.960 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catcac 5

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	2	Aaz10696 Oligonuc1
2	5	100.0	5	2	Aaz10695 Oligonuc1
3	5	100.0	5	4	Aasi4910 Melanogen
4	5	100.0	5	4	Aasi4908 Melanogen
5	5	100.0	5	8	ACD25823 Telomere-
6	5	100.0	5	8	ACD25825 Telomere-
7	5	100.0	6	7	ACA88955 Selection
8	5	100.0	7	2	Aaz10694 Oligonuc1
9	5	100.0	7	4	Aasi4911 Melanogen
10	5	100.0	7	4	Aasi4907 Melanogen
11	5	100.0	7	8	ACD25826 Melanogen
12	5	100.0	7	8	ACD25822 Telomere-
13	5	100.0	8	4	AAD02250 Direct re
14	5	100.0	9	2	AAV15899 Cyclin D
15	5	100.0	9	2	AAV22350 A promote
16	5	100.0	9	2	AAV22283 GAS compl
17	5	100.0	9	2	AAZ10692 Oligonuc1
18	5	100.0	9	4	Aasi4905 Melanogen
19	5	100.0	9	6	ABQ71504 Zinc fing
20	5	100.0	9	6	ABQ71958 Zinc fing
21	5	100.0	9	6	ABQ71922 Zinc fing
22	5	100.0	9	6	ABX03786 Human DNA
23	5	100.0	9	8	ACD25820 Telomere-

C	24	5	100.0	9	8	ADA64249	Ada64249 Zinc fing
C	25	5	100.0	9	8	ADA62652	Ada62652 Zinc fing
C	26	5	100.0	9	8	ADA64285	Ada64285 Zinc fing
C	27	5	100.0	10	2	AAQ43164	AAQ43164 Donor oli
C	28	5	100.0	10	2	AAQ71104	AAQ71104 Metlin ex
C	29	5	100.0	10	2	AAQ32625	AAQ32625 Anticance
C	30	5	100.0	10	2	AAQ97224	AAQ97224 Oligonuc1
C	31	5	100.0	10	2	AAT35734	AAT35734 Primer E1
C	32	5	100.0	10	2	AAT66073	AAT66073 (dc-da)n.
C	33	5	100.0	10	2	AAV50250	AAV50250 Yeast tag
C	34	5	100.0	10	2	AAV50271	AAV50271 Yeast tag
C	35	5	100.0	10	2	AAV50127	AAV50127 Yeast tag
C	36	5	100.0	10	2	AAV50184	AAV50184 Yeast tag
C	37	5	100.0	10	2	AAV35934	AAV35934 Primer us
C	38	5	100.0	10	2	AAV35910	AAV35910 Primer us
C	39	5	100.0	10	2	AAV18629	AAV18629 p53 seria
C	40	5	100.0	10	2	AAV73806	AAV73806 Chromopho
C	41	5	100.0	10	2	AAZ78624	AAZ78624 Human den
C	42	5	100.0	10	3	AAZ79270	AAZ79270 Human den
C	43	5	100.0	10	3	AAZ77574	AAZ77574 Human den
C	44	5	100.0	10	3	AAZ78121	AAZ78121 Human den
C	45	5	100.0	10	3	AAZ78625	AAZ78625 Human den

ALIGNMENTS

RESULT 1

ID AAZ10696 standard; DNA; 5 BP.

XX AAZ10696;

AC AAZ10696;

XX AAZ10696;

DT 23-NOV-1999 (first entry)

XX AAZ10696;

DE Oligonucleotide sequence that increases p53 activity in a cell.

XX AAZ10696;

KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;

KW UV-induced hyperproliferative disease; psoriasis; vitiligo;

KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;

KW skin cancer; ss.

OS Synthetic.

XX AAZ10696;

PN GB2336157-A.

XX AAZ10696;

PD 13-OCT-1999.

XX AAZ10696;

PF 24-MAR-1999; 99GB-00006758.

XX AAZ10696;

PR 26-MAR-1998; 98US-00048927.

XX AAZ10696;

PA (UYBO-) UNIV BOSTON.

XX AAZ10696;

PI Gilchrist BA, Yaar M, Eller M;

XX AAZ10696;

DR WPI; 1999-543520/46.

XX AAZ10696;

PT DNA fragments useful for increasing p53 activity in a cell and reducing

XX AAZ10696;

PS susceptibility to UV-induced hyperproliferative diseases.

XX AAZ10696;

CC Claim 11; Page 30; 44pp; English.

XX AAZ10696;

CC AAZ10692-97 represent DNA fragments that are used for increasing p53

XX AAZ10696;

CC activity in a cell. The oligonucleotides are UV mimetics and protect

XX AAZ10696;

CC cells against subsequent exposure to UV-irradiation or chemicals. The

XX AAZ10696;

CC oligonucleotides are useful for increasing p53 activity in a cell,

XX AAZ10696;

CC reducing the susceptibility to UV-induced hyperproliferative diseases,

XX AAZ10696;

CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,

XX AAZ10696;

CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and

XX AAZ10696;

SQ reducing susceptibility to skin cancer

XX AAZ10696;

SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.5e+08; Indels 0;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5
 |||||
 Db 1 CATAC 5

RESULT 2

AAZ10695/c
 ID AAZ10695 standard; DNA; 5 BP.

XX AC AAZ10695;

DT 23-NOV-1999 (first entry)

DE Oligonucleotide sequence that increases p53 activity in a cell.

XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
 KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
 KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
 KW skin cancer; ss.

XX OS Synthetic.

XX PN GB2336157-A.

XX PD 13-OCT-1999.

XX PF 24-MAR-1999; 99GB-00006759.

XX PR 26-MAR-1998; 98US-00048927.

XX PA (UYBO-) UNIV BOSTON.

XX PI Gilchrist BA, Year M, Eller M;

XX DR WPI; 1999-543520/46.

XX DNA fragments useful for increasing p53 activity in a cell and reducing
 susceptibility to UV-induced hyperproliferative diseases.

XX Claim 11; Page 30; 44pp; English.

XX AAZ10692-97 represent DNA fragments that are used for increasing p53
 activity in a cell. The oligonucleotides are UV mimetics and protect
 cells against subsequent exposure to UV-irradiation or chemicals. The
 oligonucleotides are useful for increasing p53 activity in a cell,
 reducing the susceptibility to UV-induced hyperproliferative diseases,
 treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,
 conjunctivitis, and UV-induced dermatoses, reducing photoaging and
 reducing susceptibility to skin cancer

XX Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 |||||
 Db 5 CATAC 1

RESULT 3

AAZ14910
 ID AAZ14910 standard; DNA; 5 BP.

XX AC AAZ14910;

XX DT 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #6.
 DE Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.

XX OS Synthetic.

XX WO200174342-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US010162.

XX PR 31-MAR-2000; 2000US-00540843.

XX PA (UYBO-) UNIV BOSTON.

XX PI Gilchrist BA, Year M, Eller M;

XX DR WPI; 2001-626338/72.

XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
 carcinoma, using specific oligonucleotides that mimic the effects of
 ultra-violet light.

XX Claim 1; Page 36; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell
 proliferation by treating cells with at least one oligonucleotide, or its
 fragment. The compounds, which have cytostatic, anti-allergic, anti-
 inflammatory, dermatological, ophthalmological, anti-psoriatic and
 immunosuppressive activities, function as 'ultra-violet mimics' to induce
 DNA repair processes (or a protective response to later exposure to
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 or a tumour necrosis factor inhibitor. Probably they mimic products of
 DNA damage, or processed DNA-damage intermediates, by inducing the p53
 pathway, resulting in transient arrest of cell growth, allowing more time
 for DNA repair to occur before cell division takes place. The method is
 especially used to treat carcinoma but may also be used to: treat other
 hyperproliferative states (e.g. psoriasis or precancerous conditions);
 reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
 allergically mediated inflammation (atopic or contact dermatitis,
 allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
 cells caused by radiation or chemicals; increase melanin production
 (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 promote apoptosis in epithelial cells that contain damaged DNA. Also
 oligonucleotides that contain non-hydrolyzable backbones are used to
 inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 sequence is melanogenesis associated oligonucleotide #6, one of the
 oligonucleotides used to inhibit mammalian epithelial cell proliferation,
 described in the method of the invention

XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 |||||
 Db 1 CATAC 5

RESULT 4

AAZ14908/c
 ID AAZ14908 standard; DNA; 5 BP.

XX AC AAZ14908;

CC pigmentosum, seborrhic keratosis, actinic keratosis, Bowen's disease, or
 CC basal cell carcinoma) and for treating or preventing pre-cancerous
 CC conditions affecting epithelial cells (such as psoriasis and atopic
 CC dermatitis) and also the types of cancers of breast, lung, liver,
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,
 CC oesophagus, stomach, and thyroid. The present sequence is a truncated
 CC telomere-like oligonucleotide of the invention
 XX
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 5; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATAC 5
 Db 5 CATAC 1
 RESULT 6
 ACD25825
 ID ACD25825 standard; DNA; 5 BP.
 XX AC ACD25825;
 XX DT 08-SEP-2003 (first entry)
 XX DE Telomere-like oligonucleotide #3.
 XX KW Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological;
 KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;
 KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;
 KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;
 KW gp-110; hyperproliferative disorder; spongiosis; blistering;
 KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrhic keratosis;
 KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;
 KW atopic dermatitis; breast cancer; lung cancer; liver cancer;
 KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;
 KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;
 KW stomach cancer; thyroid cancer.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /*mod_base= OTHER
 FT /*note= "5, phosphorylated"
 XX US2003032610-A1.
 XX PD 13-FEB-2003.
 XX PF 12-APR-2002; 2002US-00122630.
 XX PR 03-JUN-1996; 96WO-US008386.
 XX PR 26-MAR-1998; 98US-00048927.
 XX PR 31-MAR-2000; 2000US-00540843.
 XX PR 30-MAR-2001; 2001WO-US010162.
 XX (GILC/) GILCHREST B A.
 XX PA (ELLE/) ELLER M S.
 XX PA (YAAR/) YAAR M.
 XX Gilchrest BA, Eller MS, Yaar M;
 XX WPI; 2003-512221/48.
 XX DR
 XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,
 PT by administering composition having oligonucleotides that share sequence
 PT identity with human telomere overhang repeat.
 XX

PS Claim 44; Page 3; 65pp; English.
 XX The invention relates to inhibiting growth of cancer cells, which is
 CC independent of presence or activity of telomerase in cells, not requiring
 CC the presence or activity of p53 normal function in cells, or resulting in
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,
 CC involving administering a composition comprising oligonucleotides which
 CC share at least 50% sequence identity with human telomere overhang repeat,
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their
 CC contiguous portion) and is used in a method inhibiting proliferation of
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging
 CC chemicals. The method is useful for inhibiting growth of cancer cells
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in
 CC human, promoting differentiation of malignant cells in a mammal,
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,
 CC tyrosinase, TRP-1 or gp-110) indicative of differentiation of cancer
 CC cells (especially melanoma cells) in a human and for treatment of other
 CC hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis
 CC in the skin of a mammal, skin cancer in a human with xeroderma
 CC pigmentosum, seborrhic keratosis, actinic keratosis, Bowen's disease, or
 CC basal cell carcinoma) and for treating or preventing pre-cancerous
 CC conditions affecting epithelial cells (such as psoriasis and atopic
 CC dermatitis) and also the types of cancers of breast, lung, liver,
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,
 CC oesophagus, stomach, and thyroid. The present sequence is a telomere-like
 CC oligonucleotide of the invention
 XX SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 100.0%; Score 5; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATAC 5
 Db 1 CATAC 5
 RESULT 7
 ACA88955/c
 ID ACA88955 standard; DNA; 6 BP.
 XX AC ACA88955;
 XX DT 08-JUL-2003 (first entry)
 XX DE Selection and amplification of genetic markers PCR related primer #66.
 XX KW Genetic marker selection; multiplex PCR amplification;
 KW prenatal diagnostic testing; foetal sex determination;
 KW genetic identification; DNA profiling; DNA fingerprinting;
 KW forensic analysis; PCR; primer; ss.
 XX OS Homo sapiens.
 XX WO2003031646-A1.
 XX PD 17-APR-2003.
 XX PF 14-OCT-2002; 2002WO-AU001388.
 XX PR 12-OCT-2001; 2001AU-00008234.
 XX PR 12-OCT-2001; 2001AU-00008235.
 XX (UYQU) UNIV QUEENSLAND.
 XX Findlay I, Matthews PL, Mulcahy BK;
 XX WPI; 2003-381725/36.
 XX Selecting genetic markers as targets for nucleic acid sequence

PT amplification, useful for improving genetic testing, e.g. fetal sex
 PT determination, comprises selecting each of the genetic markers according
 PT to a heterozygosity index.

XX Claim 36; Page 40; 64pp; English.

CC The invention describes a method of selecting genetic markers as targets
 CC for nucleic acid sequence amplification comprising selecting each of the
 CC genetic markers according to a heterozygosity index of 0.5 or greater.
 CC Selecting and amplification of genetic markers are useful as targets for
 CC nucleic acid sequence amplification, for genetic testing or facilitating
 CC multiplex PCR amplification from limiting amounts of target nucleic acid.
 CC The methods are also useful for improving genetic diagnostic and
 CC screening methods, such as prenatal diagnostic testing, foetal sex
 CC determination or genetic identification, e.g. DNA profiling or DNA
 CC fingerprinting. The nucleic acid sequence amplification is also useful in
 CC forensic analysis of degraded, old, ancient and difficult samples that
 CC are difficult to amplify and identify. This sequence represents a PCR
 CC primer used in the selection and amplification of genetic markers

XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.1e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db |||||
 6 CATAC 2

RESULT 8

AAZ10694/C
 ID AAZ10694 standard; DNA; 7 BP.

XX AC AAZ10694;

XX DT 23-NOV-1999 (first entry)

XX DE Oligonucleotide sequence that increases p53 activity in a cell.

XX KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
 KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
 KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
 KW skin cancer; ss.

XX OS Synthetic.

XX PN GB2336157-A.

XX PD 13-OCT-1999.

XX PF 24-MAR-1999; 99GB-00006758.

XX PR 26-MAR-1998; 98US-00048927.

XX PA (UYBO-) UNIV BOSTON.

XX PI Gilchrest BA, Yaar M, Eller M;

XX PS WPI; 1999-543520/46.

XX DR DNA fragments useful for increasing p53 activity in a cell and reducing
 PT susceptibility to UV-induced hyperproliferative diseases.

XX PS Claim 11; Page 30; 44pp; English.

XX CC AAZ10692-97 represent DNA fragments that are used for increasing p53
 CC activity in a cell. The oligonucleotides are UV mimetics and protect
 CC cells against subsequent exposure to UV-irradiation or chemicals. The
 CC oligonucleotides are useful for increasing p53 activity in a cell,
 CC reducing the susceptibility to UV-induced hyperproliferative diseases,
 CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,

CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and
 CC reducing susceptibility to skin cancer

XX SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db |||||
 6 CATAC 2

RESULT 9

AAS14911/C

ID AAS14911 standard; DNA; 7 BP.

XX AC AAS14911;

XX DT 14-FEB-2002 (first entry)

XX DE Melanogenesis associated oligonucleotide #7.

XX KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= a
 FT /note= "Phosphorylated"

XX PN WO200174342-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US010162.

XX PR 31-MAR-2000; 2000US-00540843.

XX PA (UYBO-) UNIV BOSTON.

XX PI Gilchrest BA, Yaar M, Eller M;

XX PS WPI; 2001-626338/72.

XX DR Inhibiting proliferation of epithelial cells, useful e.g. for treating
 PT carcinoma, using specific oligonucleotides that mimic the effects of
 PT ultra-violet light.

XX PS Claim 1; Page 38; 74pp; English.

XX CC The invention describes inhibition of mammalian epithelial cell
 CC proliferation by treating cells with at least one oligonucleotide, or its
 CC fragment. The compounds, which have cytostatic, anti-allergic, anti-
 CC inflammatory, dermatological, ophthalmological, anti-psoriatic and
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce
 CC DNA repair processes (or a protective response to later exposure to
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53
 CC pathway, resulting in transient arrest of cell growth, allowing more time
 CC for DNA repair to occur before cell division takes place. The method is
 CC especially used to treat carcinoma but may also be used to treat other
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat

CC allergically mediated inflammation (atopic or contact dermatitis;
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
 CC cells caused by radiation or chemicals; increase melanin production
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also
 CC oligonucleotides that contain non-hydrolyzable backbones are used to
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 CC sequence is melanogenesis associated oligonucleotide #7, one of the
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,
 CC described in the method of the invention

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 5; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db 6 CATAC 2
 |||||
 |||||

RESULT 10
 AAS14907/c
 ID AAS14907 standard; DNA; 7 BP.
 XX AC AAS14907;
 XX DT 14-FEB-2002 (first entry)
 XX DE Melanogenesis associated oligonucleotide #3.
 XX KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.
 XX OS Synthetic.
 XX WO200174342-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US010162.
 XX PR 31-MAR-2000; 2000US-00540843.
 XX PA (UYBO-) UNIV BOSTON.
 XX PI Gilchrist BA, Yaar M, Eller M;
 XX WPI; 2001-626338/72.
 XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
 XX carcinoma, using specific oligonucleotides that mimic the effects of
 XX ultra-violet light.
 XX Claim 1; Page 36; 74pp; English.
 XX The invention describes inhibition of mammalian epithelial cell
 XX proliferation by treating cells with at least one oligonucleotide, or its
 XX fragment. The compounds, which have cytostatic, anti-allergic, anti-
 XX inflammatory, dermatological, ophthalmological, anti-psoriatic and
 XX immunosuppressive activities, function as 'ultra-violet mimics' to induce
 XX DNA repair processes (or a protective response to later exposure to
 XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 XX or a tumour necrosis factor inhibitor. Probably they mimic products of
 XX DNA damage, or processed DNA-damage intermediates, by inducing the p53
 XX pathway, resulting in transient arrest of cell growth, allowing more time
 XX for DNA repair to occur before cell division takes place. The method is
 XX especially used to treat carcinoma but may also be used to: treat

CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
 CC allergically mediated inflammation (atopic or contact dermatitis;
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
 CC cells caused by radiation or chemicals; increase melanin production
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also
 CC oligonucleotides that contain non-hydrolyzable backbones are used to
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 CC sequence is melanogenesis associated oligonucleotide #3, a truncated
 CC version of the oligonucleotide shown in AAS14906, one of the
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,
 CC described in the method of the invention

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 5; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db 6 CATAC 2
 |||||
 |||||

RESULT 11
 ACD25826/c
 ID ACD25826 standard; DNA; 7 BP.
 XX AC ACD25826;
 XX DT 08-SEP-2003 (first entry)
 XX DE Melanogenic telomere-like oligonucleotide #1.
 XX KW Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological;
 KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;
 KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;
 KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;
 KW gp-1100; hyperproliferative disorder; spongiolysis; blistering;
 KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;
 KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;
 KW atopic dermatitis; breast cancer; lung cancer; liver cancer;
 KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;
 KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;
 KW stomach cancer; thyroid cancer.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 XX modified_base 1
 XX /*tag= a
 XX /mod_base= OTHER
 XX /note= '5, phosphorylated'
 XX US2003032610-A1.
 XX PD 13-FEB-2003.
 XX PF 12-APR-2002; 2002US-00122630.
 XX PR 03-JUN-1996; 96WO-US008386.
 XX PR 26-MAR-1998; 98US-00048927.
 XX PR 31-MAR-2000; 2000US-00540843.
 XX PR 30-MAR-2001; 2001WO-US010162.
 XX (GILC/) GILCHREST B A.
 XX (ELLE/) ELLER M S.
 XX (YAAR/) YAAR M.
 XX Gilchrist BA, Eller MS, Yaar M;
 XX WPI; 2003-512221/48.

XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,
 PT by administering composition having oligonucleotides that share sequence
 PT identity with human telomere overhang repeat.

XX Claim 44; Page 18; 65pp; English.

XX The invention relates to inhibiting growth of cancer cells, which is
 CC independent of presence or activity of telomerase in cells, not requiring
 CC the presence or activity of p53 normal function in cells, or resulting in
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,
 CC involving administering a composition comprising oligonucleotides which
 CC share at least 50% sequence identity with human telomere overhang repeat,
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their
 CC contiguous portion) and is used in a method inhibiting proliferation of
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging
 CC chemicals. The method is useful for inhibiting growth of cancer cells
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in
 CC human, promoting differentiation of malignant cells in a mammal,
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer
 CC cells (especially melanoma cells) in a human and for treatment of other
 CC hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis
 CC in the skin of a mammal, skin cancer in a human with xeroderma
 CC pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or
 CC basal cell carcinoma) and for treating or preventing pre-cancerous
 CC conditions affecting epithelial cells (such as psoriasis and atopic
 CC dermatitis) and also the types of cancers of breast, lung, liver,
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,
 CC oesophagus, stomach, and thyroid. The present sequence is a melanogenic
 CC telomere-like oligonucleotide of the invention

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db |||||
 6 CATAC 2

RESULT 12
 ACD25822/c

ID ACD25822 standard; DNA; 7 BP.

AC ACD25822;

DT 08-SEP-2003 (first entry)

DE Telomere-like oligonucleotide #1 truncated version #1.

XX Telomere; ss; probe; cytostatic; human; antiproliferative; dermatological;
 KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;
 KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;
 KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;
 KW gp-1100; hyperproliferative disorder; spongiosis; blistering;
 KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;
 KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;
 KW atopic dermatitis; breast cancer; lung cancer; liver cancer;
 KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;
 KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;
 KW stomach cancer; thyroid cancer.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a

FT /mod_base= OTHER
 FT /note= '5', phosphorylated"
 XX US2003032610-A1.

XX 13-FEB-2003.

XX 12-APR-2002; 2002US-00122630.

XX 03-JUN-1996; 96WO-US0008386.

XX 26-MAR-1998; 98US-00048927.

XX 31-MAR-2000; 2000US-00540843.

XX 30-MAR-2001; 2001WO-US010162.

XX (GILC/) GILCHREST B A.

XX (ELLE/) ELLER M S.

XX (YAAR/) YAAR M.

XX Gilchrest BA, Eller MS, Yaar M;

XX WPI; 2003-512221/48.

XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,

PT by administering composition having oligonucleotides that share sequence

PT identity with human telomere overhang repeat.

XX Claim 44; Page 6; 65pp; English.

XX The invention relates to inhibiting growth of cancer cells, which is
 CC independent of presence or activity of telomerase in cells, not requiring
 CC the presence or activity of p53 normal function in cells, or resulting in
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,
 CC involving administering a composition comprising oligonucleotides which
 CC share at least 50% sequence identity with human telomere overhang repeat,
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their
 CC contiguous portion) and is used in a method inhibiting proliferation of
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging
 CC chemicals. The method is useful for inhibiting growth of cancer cells
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in
 CC human, promoting differentiation of malignant cells in a mammal,
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer
 CC cells (especially melanoma cells) in a human and for treatment of other
 CC hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis
 CC in the skin of a mammal, skin cancer in a human with xeroderma
 CC pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or
 CC basal cell carcinoma) and for treating or preventing pre-cancerous
 CC conditions affecting epithelial cells (such as psoriasis and atopic
 CC dermatitis) and also the types of cancers of breast, lung, liver,
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,
 CC oesophagus, stomach, and thyroid. The present sequence is a truncated
 CC telomere-like oligonucleotide of the invention

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 Db |||||
 6 CATAC 2

RESULT 13

AAD02250

ID AAD02250 standard; DNA; 8 BP.

XX AAD02250;

DT 28-MAR-2001 (first entry)

XX DE Direct repeat sequence that binds to SB protein.
XX KW Sleeping Beauty; SB; AdSB10; adenovirus; transposase;
XX KW non-integrating viral vector; cytostatic; anti-diabetic; cardiatic;
KW neuroprotective; genetic disease; gene therapy; therapy; cancer;
KW cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;
KW genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
XX OS Unidentified.
XX OS WO200068399-A2.
XX PN 16-NOV-2000.
XX PD
XX PF 11-MAY-2000; 2000WO-US012827.
XX PR 11-MAY-1999; 99US-0133569P.
XX PR (MINU) UNIV MINNESOTA.
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PA (MCIV/) MCIVOR R S.
XX PA (HACK/) HACKETT P B.
XX PA (AGUI/) AGUILAR-CORDOVA E.
XX PI Mcivor RS, Hackett PB, Aguilar-Cordova E;
XX DR WPI; 2001-024870/03.
XX DR
XX PT Non-integrating (adenovirus-based) viral vectors useful in gene therapy,
XX PT especially for treating patients suffering from a genetic disease, e.g.
XX PT cystic fibrosis, diabetes, cardiovascular disease, cancer or brain
XX PT malfunction.
XX PS Disclosure; Page 14; 62pp; English.
XX CC The patent discloses non-integrating viral vectors comprising a
XX CC polynucleotide flanked by inverted repeats that bind a transposase, a
XX CC transposase-encoding polynucleotide operably linked to a regulatory
XX CC sequence comprising an operator, that alters expression of the
XX CC transposase-encoding polynucleotide. Transposon sequences can integrate
XX CC into genomic DNA whether or not the cell is dividing. AdSB10 is a SB
XX CC (Sleeping Beauty) transposase-transducing adenoviral non-integrating
XX CC vector. The non-integrating viral vectors are useful for treating genetic
XX CC disease characterised by subnormal production of a polypeptide or RNA,
XX CC e.g. for replacement of a defective gene, delivery of a polypeptide drug
XX CC or supplementation of a metabolic activity. These genetic diseases
XX CC include cystic fibrosis, diabetes, cardiovascular disease, cancer or
XX CC brain malfunction. The non-integrating viral vectors are useful as
XX CC nucleic acid delivery systems, e.g. for genome analysis or gene therapy
XX CC and can also be used for applications that involve long-term production
XX CC of a polypeptide. The non-integrating viral vectors are also useful for
XX CC creating transgenic host cells that provide normal cells with protection
XX CC against toxic side effects of chemotherapy. The sequence of the present
XX CC invention is a direct repeat sequence that binds to SB protein
XX CC
XX SQ Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db |||||
2 CATAC 6

RESULT 14
AAV15899/c
ID AAV15899 standard; DNA; 9 BP.
XX
XX AC AAV15899;
XX

DT 26-MAY-1998 (first entry)
XX DE Cyclin D transcription factor DMP1 nonamer consensus sequence.
XX KW cyclin D transcription factor; binding affinity; D-type cyclin; probe;
KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
KW nonamer consensus sequence; ss.
XX OS Mus musculus.
XX OS Homo sapiens.
XX PN WO9743415-A1.
XX XX 20-NOV-1997.
XX PF 16-MAY-1997; 97WO-US008480.
XX PR 16-MAY-1996; 96US-0017815P.
XX PR 16-MAY-1996; 96US-00648837.
XX PR 15-MAY-1997; 97US-00257071.
XX PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX XX Hirai H, Sherr CJ, Inoue K;
XX PI WPI; 1998-008884/01.
XX DR
XX XX Cyclin D transcription factor and related DNA - can be used to develop
XX PT products for treatment of, e.g. cancer.
XX PS Claim 3; Page 99; 120pp; English.
XX CC This is a nonamer consensus sequence of a cyclin D transcription factor
XX CC DMP1. DMP1 is an amino acid polymer which has binding affinity for a D-
XX CC type cyclin, in vitro, and for a specific DNA nucleotide sequence and is
XX CC a transcription factor involved in the activation of genes that prevent
XX CC cell proliferation. The DMP1 nucleic acid is operatively linked to an
XX CC expression control sequence in an expression vector. The expression
XX CC vector has a transcription control sequence comprising this nonamer
XX CC sequence operably associated with a recombinant gene or a cassette
XX CC insertion site for a recombinant gene. The vector is homologously
XX CC recombined in a chromosome of a transgenic animal. A probe or a
XX CC competitor in DMP1 transactivation assays is designed based on this
XX CC nonamer sequence. The presence of activity of DMP1 can be determined by
XX CC detecting binding of DMP1 and a probe by contacting a biological sample
XX CC from a mammal with the probe under conditions that allow binding of the
XX CC probe to DMP1, where the probe contains the core sequence GTA, and where
XX CC the presence or activity of DMP1 is suspected in the sample. DMP1 can
XX CC function as a cell cycle inhibitor when expressed in a tumour cell.
XX CC Modulating the expression of DMP1 can be used to treat tumours and other
XX CC cancers. DMP1 can also be used for controlling expression of heterologous
XX CC proteins. Antisense sequences and ribozymes can be used to inhibit
XX CC expression of the transcription factor. Detecting the level and activity
XX CC of DMP1 in cells is useful for detection of cancer cells or
XX CC dysproliferative cells
XX CC
XX SQ Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db |||||
8 CATAC 4

RESULT 15
AAV22350/c
ID AAV22350 standard; RNA; 9 BP.
XX
XX AC AAV22350;
XX

DT 29-JUN-1998 (first entry)
 XX
 DE
 XX
 XX
 KW A promoter regulatory motif found in the utrons of the invention.
 KW 3' untranslated region; UTR; inhibition; gene expression; ICAM-7;
 KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
 KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;
 KW HIV gene expression; transplant rejection; treatment; autoimmune disease;
 KW inflammatory disease; ss.
 XX
 OS Unidentified.
 XX
 XX WO9744450-A1.
 FN
 XX
 XX
 PD 27-NOV-1997.
 XX
 XX 21-MAY-1997; 97WO-US009459.
 PF
 XX 21-MAY-1996; 96US-00646789.
 XX
 XX (UYVA) UNIV YALE.
 PA
 XX
 XX Peyman JA;
 FI
 XX
 XX WPI; 1998-018505/02.
 DR
 XX
 XX
 XX Utrons, RNA molecules containing promoter regulatory motifs - useful to
 PT suppress express expression from promoter of interest, specifically TSU
 PT nucleic acid suppression of MHC Class I and II gene expression.
 XX
 XX Claim 20; Page 20; 200pp; English.
 FS
 XX
 XX The present sequence represents a promoter regulatory element, found in
 CC the utrons of the invention. Utrons are from, or are homologous to, the
 CC 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a
 CC cellular response by sequence specific interactions. The utron is able to
 CC suppress constitutive and interferon-gamma (IFN-gamma) induced major
 CC histocompatibility complex (MHC) class I and class II antigen expression
 CC and expression of other antigens, the gene promoters of which contain
 CC related sequence motifs that are stimulated by the same factors which
 CC stimulate MHC class I and class II antigen expression. Such utrons can be
 CC used to regulate gene expression in a subject, e.g. a human or a cell in
 CC vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2, Fc
 CC gamma R, IL-2 or HIV gene expression. They can be used to inhibit
 CC transplant rejection, or treat an autoimmune or inflammatory disease or
 CC disorder
 XX
 SQ Sequence 9 BP; 3 A; 0 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 100.0%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATAC 5
 Db 5 CATAC 1

Search completed: August 11, 2004, 17:56:32
 Job time : 76.5914 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 16:50:49 ; Search time 598.548 Seconds
(without alignments)
249.455 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catac 5

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_estl.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estcom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	13	14	CF543283 S014680-0
2	5	100.0	14	12	BM398220 5009-0-42
3	5	100.0	16	9	AI424037 tf51h06.x
4	5	100.0	16	9	AI685758 tu37g09.x

5	5	100.0	16	9	AI721735
6	5	100.0	16	12	BG928185
7	5	100.0	17	12	BG929060
8	5	100.0	17	13	BQ595683
9	5	100.0	17	13	C21103
10	5	100.0	18	12	BM3397954
11	5	100.0	19	9	AA977115
12	5	100.0	19	9	AI120725
13	5	100.0	19	9	AI747751
14	5	100.0	19	13	BX551013
15	5	100.0	19	13	C00646
16	5	100.0	19	13	AZ341880
17	5	100.0	19	28	AZ345849
18	5	100.0	19	28	AZ355195
19	5	100.0	19	28	AZ406137
20	5	100.0	19	28	AZ422163
21	5	100.0	19	28	AZ434551
22	5	100.0	19	28	AZ464990
23	5	100.0	19	28	AZ486152
24	5	100.0	19	28	AZ579566
25	5	100.0	19	28	AZ614702
26	5	100.0	19	28	AZ626685
27	5	100.0	19	28	AZ645469
28	5	100.0	19	28	AZ647364
29	5	100.0	19	28	AZ759906
30	5	100.0	19	28	AZ766086
31	5	100.0	19	28	AZ799396
32	5	100.0	19	28	AZ815067
33	5	100.0	19	28	AZ817238
34	5	100.0	19	28	AZ839614
35	5	100.0	19	28	AZ864822
36	5	100.0	19	28	AZ942806
37	5	100.0	19	28	AZ948421
38	5	100.0	19	28	AZ949895
39	5	100.0	19	28	AZ953217
40	5	100.0	19	28	AZ987324
41	5	100.0	19	28	AZ990856
42	5	100.0	20	9	AB088508
43	5	100.0	20	13	BQ593049
44	5	100.0	20	28	AZ336039
45	5	100.0	20	28	AZ359199

ALIGNMENTS

RESULT 1
CF543283
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF543283 13 bp mRNA linear EST 22-SEP-2003
S014680-024-030-D02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-030-D02 5-PRIME, mRNA sequence.

CF543283 1 GI:34891723
EST.
Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radeilof, J.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Description

CF543283 S014680-0
BM398220 5009-0-42
AI424037 tf51h06.x
AI685758 tu37g09.x

AI685758
 LOCUS tu37909.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'
 DEFINITION similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 ES CENTRAL
 SEQUENCE MOTIF PROTEIN 1 ; contains element LTR4 repetitive element
 ;, mRNA sequence.
 ACCESSION AI685758
 VERSION AI685758.1 GI:4897052
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: czapbs-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
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 /db_xref="taxon:9606"
 /clone="IMAGE:2253280"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr28"
 /notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneIDs
 985608-986759, 1101192-1101959, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 100.0%; Score 5; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATAC 5
 Db |||||
 5 CATAC 9

RESULT 5
 AI721735
 LOCUS AI721735
 DEFINITION f31908.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
 IMAGE:3723038 3', similar to SW:YM14_PART2 P15615 HYPOTHETICAL 47.2
 KD PROTEIN ;, mRNA sequence.
 ACCESSION AI721735
 VERSION AI721735.1 GI:5040064
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

Query Match 100.0%; Score 5; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATAC 5
 Db |||||
 5 CATAC 9

RESULT 5
 AI721735
 LOCUS AI721735
 DEFINITION f31908.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
 IMAGE:3723038 3', similar to SW:YM14_PART2 P15615 HYPOTHETICAL 47.2
 KD PROTEIN ;, mRNA sequence.
 ACCESSION AI721735
 VERSION AI721735.1 GI:5040064
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
 Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
 Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 WashU Zebrafish EST Project 1998
 Other_ESTs: fc31908.y1
 Unpublished (1998)
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@watson.wustl.edu
 cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Resourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: T7 ET from Amersham
 High quality sequence stop: 1.
 FEATURES
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 1. 16
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 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:3723038"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="XL1-blue MRF"
 /clone_lib="Zebrafish WashU MPIMG EST"
 /notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
 strand cDNA was primed with a Not I - oligo (drr)15 primer
 [5'pgactagttctagatccgagccgcgccttttttttttt3'];
 double-stranded cDNA was ligated to Sal I adaptors (BRL),
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."

Query Match 100.0%; Score 5; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATAC 5
 Db |||||
 9 CATAC 13

RESULT 6
 BG928185

LOCUS BG928185 16 bp mRNA linear EST 06-NOV-2001
 DEFINITION HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG928185
 VERSION BG928185.1 GI:14322708
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
 JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 MEDLINE 21482651
 PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UW2109

GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay_kumar-1@gsk.com
 Seq primer: T7.

FEATURES
 source
 1..16
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

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 Best Local Similarity 100.0%; Pred. NO. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 8 CATAC 12

RESULT 7
 BG929060
 LOCUS HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG929060
 ACCESSION BG929060.1 GI:143233583
 VERSION BG929060
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND OSTEOARTHRITIC CARTILAGE cDNA LIBRARIES
 JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 MEDLINE 21482651
 PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UW2109

GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay_kumar-1@gsk.com
 Seq primer: T7.

FEATURES
 source
 1..17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN

Query Match 100.0%; Score 5; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
 Db 6 CATAC 10

RESULT 8

BQ595683
 LOCUS E012692-024-022-H17-SP6 MP1Z-ADIS-024-developing root Beta vulgaris cDNA clone 024-022-H17 5-PRIME, mRNA sequence.
 DEFINITION BQ595683
 ACCESSION BQ595683.1 GI:26125266
 VERSION BQ595683
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Herwig,A., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 22 row: H column: 17
 Seq primer: SP6; CATACGATTTAGGTGACACTATAG.

FEATURES
 source
 1..17
 Location/Qualifiers
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:191174"
 /db_xref="taxon:161934"
 /clone="024-022-H17"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-developing root"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

```

b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
orientation:
SP6-Sall-CCACCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 3 CATAC 7

RESULT 9
C21103
LOCUS
DEFINITION
HMG50002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
sequence.
C21103
VERSION
C21103.1 GI:1622213
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Okubo, K.
TITLE
BodyMap; human gene expression database
JOURNAL
Unpublished (1995)
COMMENT
Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel.: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBEJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/notes="One or more human adult tissue"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 9 CATAC 13

RESULT 10
BM397954
LOCUS
DEFINITION
5009-0-39-G08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM397954
VERSION
BM397954.1 GI:18198022
KEYWORDS
EST.

```

```

Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
source
Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 1 CATAC 5

RESULT 11
AA977115/c
LOCUS
DEFINITION
Oq24c08.s1 NCI-CGAP GC4 Homo sapiens cDNA clone IMAGE:1587278 3'
similar to TR:Q69566 Q69566 ; mRNA sequence.
ACCESSION
AA977115
VERSION
AA977115.1 GI:3154561
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Emmert-Buck, M.D., Ph.D.
TITLE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
 /clone="IMAGE:1587278"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_GC4"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
 |||||
 Db 13 CATAC 9

RESULT 12

LOCUS

DEFINITION ub72b11.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ; mRNA sequence.

ACCESSION AI120725

VERSION AI120725

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 Authors: Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:905729

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. .19

Location/Qualifiers

/organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1383261"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"

/clone_lib="Soares_mammary_gland_NMLMG"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was

ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

|||||

Db 7 CATAC 11

RESULT 13

LOCUS

DEFINITION

AI747751 19 bp mRNA linear EST 22-JUN-1999
 ul21h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ; mRNA sequence.

ACCESSION AI747751

VERSION AI747751

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 Authors: Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:995933

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

FEATURES

source

1. .19

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:2088249"

/dev_stage="embryo, 14 dpc"

/lab_host="DH10B"

/clone_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTTGGCCTACTGG], digested and cloned into distinct DraIII

sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site

CACCATGTG). XhoI should be used to isolate the cDNA

insert. Size selection was performed to exclude fragments

<1.5kb. Library constructed by Dr. Sumio Sugano

(University of Tokyo Institute of Medical Science).

Custom primers for sequencing: 5' end primer

CTTCTGCTCTAAAAGCTGGC and 3' end primer

CGACCTGCAGCTCGAGCACA."

ORIGIN

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Query Match      100.0%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
    |||||
Db 17 CATAC 13

RESULT 14
BX551013/c
LOCUS
DEFINITION BX551013 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tsel16a12_glc, mRNA sequence.
ACCESSION BX551013
VERSION BX551013.1 GI:33374827
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
            Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 19)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
          Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
          Pathogen Sequencing Unit
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J. Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix gic are reverse primer reads starting at 5'
          end of the cDNA all pic reads are from
          the 3' end.
FEATURES             Location/Qualifiers
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                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tsel16a12_glc"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /notes="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

ORIGIN

Query Match      100.0%; Score 5; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
    |||||
Db 12 CATAC 8

RESULT 15
C00646/c
LOCUS
DEFINITION HUMGS0008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
sequence.
ACCESSION C00646

```

```

VERSION C00646.1 GI:1432876
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Okubo, K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo, K.
          Institute for Molecular and Cellular Biol
          Osaka University
          1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
          Tel: 06-877-5111 (ex.3315)
          Email: kousaku@imcb.osaka-u.ac.jp
          We are not submitting the same cDNA sequence redundantly to DBJ
          since 1993. For the abundance information of clones with this
          sequence in this library and as well as in other 3'-directed
          libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
          sequences of the clones represented by this GS sequences is also
          found there.
FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
                     /clone_lib="Human adult (K.Okubo)"
                     /note="One or more human adult tissue"

ORIGIN

Query Match      100.0%; Score 5; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
    |||||
Db 18 CATAC 14

Search completed: August 11, 2004, 18:58:43
Job time : 607.215 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:57:26 ; Search time 15 Seconds
(without alignments)
184.984 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 carac 5

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979484

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5	100.0	5	3	US-08-855-372B-20
C 2	5	100.0	5	3	US-09-048-927-4
C 3	5	100.0	5	4	US-09-498-851-20
C 4	5	100.0	7	1	US-08-615-170-10
C 5	5	100.0	7	1	US-08-615-170-12
C 6	5	100.0	7	3	US-09-048-927-3
C 7	5	100.0	8	4	US-09-142-593-11
C 8	5	100.0	8	4	US-09-927-886-17
C 9	5	100.0	9	2	US-08-583-276-1
C 10	5	100.0	9	3	US-08-646-789A-8
C 11	5	100.0	9	3	US-08-646-789A-80
C 12	5	100.0	9	3	US-09-048-927-1
C 13	5	100.0	9	4	US-09-319-648-68
C 14	5	100.0	9	4	US-09-989-789-623
C 15	5	100.0	9	4	US-09-989-789-2220
C 16	5	100.0	9	4	US-09-989-789-2256
C 17	5	100.0	10	1	US-09-282-790-37
C 18	5	100.0	10	1	US-09-721-777-19
C 19	5	100.0	10	1	US-08-335-565A-27
C 20	5	100.0	10	1	US-08-250-951-1
C 21	5	100.0	10	1	US-08-232-233-1
C 22	5	100.0	10	1	US-08-222-177A-422
C 23	5	100.0	10	1	US-08-351-748-23
C 24	5	100.0	10	1	US-08-351-748-25
C 25	5	100.0	10	1	US-08-202-927-25
C 26	5	100.0	10	1	US-08-430-536A-23
C 27	5	100.0	10	1	US-08-430-536A-25

C 28	5	100.0	10	1	US-08-171-718-45	Sequence 45, Appl
C 29	5	100.0	10	2	US-08-703-601-1	Sequence 1, Appl
C 30	5	100.0	10	2	US-08-684-547-23	Sequence 23, Appl
C 31	5	100.0	10	2	US-08-684-547-25	Sequence 25, Appl
C 32	5	100.0	10	3	US-08-469-318-174	Sequence 174, App
C 33	5	100.0	10	3	US-08-468-609A-174	Sequence 174, App
C 34	5	100.0	10	3	US-08-478-087-45	Sequence 45, Appl
C 35	5	100.0	10	3	US-09-063-450-24	Sequence 24, Appl
C 36	5	100.0	10	3	US-09-063-450-33	Sequence 33, Appl
C 37	5	100.0	10	3	US-09-123-638-1	Sequence 1, Appl
C 38	5	100.0	10	3	US-08-646-695-30	Sequence 30, Appl
C 39	5	100.0	10	3	US-08-875-533-31	Sequence 31, Appl
C 40	5	100.0	10	4	US-08-446-872A-174	Sequence 174, App
C 41	5	100.0	10	4	US-09-724-753-1	Sequence 1, Appl
C 42	5	100.0	10	4	US-08-762-227A-174	Sequence 174, App
C 43	5	100.0	10	4	US-09-475-947A-23	Sequence 23, Appl
C 44	5	100.0	10	4	US-09-427-834A-34	Sequence 34, Appl
C 45	5	100.0	10	4	US-09-445-388A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-855-372B-20/c
; Sequence 20, Application US/08855372B
; Patent No. 6090549
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagn
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,372B
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: yes
US-08-855-372B-20

Query Match 100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 5 CATAC 1

RESULT 2

US-09-048-927-4/c
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-4

Query Match 100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+08; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 5 CATAC 1

RESULT 3

US-09-498-851-20/c
; Sequence 20, Application US/09498851
; Patent No. 6440671
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous
; TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,851
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/855,372
; FILING DATE: 13-MAY-97
; APPLICATION NUMBER: U.S. 08/587,332

; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6440671 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: Yes
US-09-498-851-20

Query Match 100.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+08; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATAC 5
Db 5 CATAC 1

RESULT 4

US-08-615-170-10
; Sequence 10, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anthony
; APPLICANT: MAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.
; APPLICANT: LARKIN, Sarah B.
; TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01526
; FILING DATE: 06-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/191,493
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 2307U-053120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..7
; OTHER INFORMATION: /standard_name= "Sph-II binding
; OTHER INFORMATION: site in SV40"
US-08-615-170-10

Query Match          100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 7.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

RESULT 5
US-08-615-170-12
; Sequence 12, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anchoy
; APPLICANT: MAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.
; APPLICANT: LARKIN, Sarah B.
; TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01526
; FILING DATE: 06-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/191,493
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 2307U-053120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..7
; OTHER INFORMATION: /standard_name= "Rat beta-Myosin
; OTHER INFORMATION: Heavy Chain M-CAT binding element "
US-08-615-170-12

Query Match          100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 7.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

RESULT 6
US-09-048-927-3/c
; Sequence 3, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Vaar, Mina
; APPLICANT: Ellser, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-3

Query Match          100.0%; Score 5; DB 3; Length 7;
Best Local Similarity 100.0%; Pred.No. 7.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 6 CATAC 2

RESULT 7
US-09-142-593-11
; Sequence 11, Application US/09142593
; Patent No. 6489458
; GENERAL INFORMATION:
; APPLICANT: HACKETT ET AL.
; TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
; TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,593
; FILING DATE: 10-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/040,664
; FILING DATE: 11-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,868
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/065,303
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04687
; FILING DATE: 11-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 110.00450101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-142-593-11

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Query Match      100.0%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.5e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CATAC 5
        |||||
Db       2 CATAC 6

```

```

RESULT 8
US-09-927-886-17
; Sequence 17, Application US/09927886
; Patent No. 6613752
; GENERAL INFORMATION:
; APPLICANT: Kay, Mark A.
; TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
; TITLE OF INVENTION: Sleeping Beauty Transposon System
; FILE REFERENCE: STAN-160CIP
; CURRENT APPLICATION NUMBER: US/09/927,886
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/162,279
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 09/440,301
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: transposon repeat sequence
US-09-927-886-17

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Query Match      100.0%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.5e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CATAC 5
        |||||

```

Db 2 CATAC 6

```

RESULT 9
US-08-583-276-1/c
; Sequence 1, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; APPLICANT: Tolstoshev, Paul
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DM4 V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712
; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 bases
; TYPE: nucleic acid
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: Genomic DNA
US-08-583-276-1

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Query Match      100.0%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CATAC 5
        |||||
Db       8 CATAC 4

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RESULT 10
US-08-646-789A-8/c
; Sequence 8, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-8

Query Match 100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 CATAC 5
Db 5 CATAC 1

RESULT 11
US-08-646-789A-80/c
Sequence 80, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-646-789A-80

Query Match 100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 CATAC 5
Db 5 CATAC 1

RESULT 12
US-09-048-927-1/c
Sequence 1, Application US/09048927
Patent No. 6147056
GENERAL INFORMATION:
APPLICANT: Gilchrist, Barbara A.
APPLICANT: Yaar, Mina
APPLICANT: Eller, Mark
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA Fragment
US-09-048-927-1

Query Match 100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 CATAC 5
Db 7 CATAC 3

RESULT 13
US-09-319-648-68
Sequence 68, Application US/09319648
Patent No. 6451530
GENERAL INFORMATION:
APPLICANT: Hawkins, Mary
TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
Formation for Detection of Nucleic Acid Hybridization
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/319,648
FILING DATE: 30-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,844
FILING DATE: 13-DEC-1996

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; APPLICATION NUMBER: WO PCT/US97/22448
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fang, Carol
; REGISTRATION NUMBER: 48,631
; REFERENCE/DOCKET NUMBER: 015280-288100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
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Db      3 CATAC 7

RESULT 14
US-09-989-789-623
; Sequence 623, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 623
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-623

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
      |||||
Db      3 CATAC 7

Search completed: August 11, 2004, 19:33:23
Job time : 17 secs
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; APPLICATION NUMBER: WO PCT/US97/22448
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fang, Carol
; REGISTRATION NUMBER: 48,631
; REFERENCE/DOCKET NUMBER: 015280-288100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
      |||||
Db      3 CATAC 7

RESULT 14
US-09-989-789-623
; Sequence 623, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 623
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-623

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
      |||||
Db      2 CATAC 6

RESULT 15
US-09-989-789-2220/c
; Sequence 2220, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2220
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 19:00:04 ; Search time 72.0968 Seconds
(without alignments)
340.279 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catac 5

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 2263564

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA: *

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
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C 2	5	100.0	5	15	US-10-122-630-6
C 3	5	100.0	5	15	US-10-122-633-4
C 4	5	100.0	5	15	US-10-122-633-6
C 5	5	100.0	7	13	US-10-027-632-178029
C 6	5	100.0	7	13	US-10-027-632-178043
C 7	5	100.0	7	15	US-10-122-630-3
C 8	5	100.0	7	15	US-10-122-630-7
C 9	5	100.0	7	15	US-10-122-633-3
C 10	5	100.0	7	15	US-10-122-633-7
C 11	5	100.0	7	16	US-10-027-632-178029
C 12	5	100.0	7	16	US-10-027-632-178043
C 13	5	100.0	8	9	US-09-142-593-11
C 14	5	100.0	8	9	US-09-927-886-17

Sequence 6, Appli
Sequence 1138, Ap
Sequence 11, Appl
Sequence 224, App
Sequence 11, Appl
Sequence 5, Appli
Sequence 17, Appl
Sequence 623, App
Sequence 2220, Ap
Sequence 2256, Ap
Sequence 623, App
Sequence 2220, Ap
Sequence 2256, Ap
Sequence 623, App
Sequence 2220, Ap
Sequence 2256, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 32, Appl
Sequence 13, Appl
Sequence 3, Appli
Sequence 16, Appl
Sequence 31, Appl
Sequence 622, App
Sequence 636, App
Sequence 1338, Ap
Sequence 1341, Ap
Sequence 1342, Ap
Sequence 1343, Ap
Sequence 31, Appli

8 9 US-09-861-014-6
8 13 US-10-314-578-1138
8 15 US-10-263-159-11
8 15 US-10-128-560-224
8 15 US-10-191-698-11
8 17 US-10-132-914-5
8 17 US-10-608-516-17
9 9 US-09-989-789-623
9 9 US-09-989-789-2220
9 9 US-09-989-789-2256
9 10 US-09-990-186-623
9 10 US-09-990-186-2220
9 10 US-09-989-994-623
9 10 US-09-989-994-2220
9 15 US-10-122-630-1
9 15 US-10-122-633-1
9 15 US-10-096-596-32
9 16 US-10-378-558A-13
9 17 US-10-427-629-3
10 8 US-08-935-377-16
10 9 US-09-822-250-16
10 9 US-09-398-399-31
10 9 US-09-989-789-622
10 9 US-09-989-789-636
10 9 US-09-989-789-1338
10 9 US-09-989-789-1341
10 9 US-09-989-789-1342
10 9 US-09-989-789-1343
10 9 US-09-899-381-31

ALIGNMENTS

RESULT 1
US-10-122-630-4/c
; Sequence 4, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilcrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Vaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-4

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 5 CATAC 1

RESULT 2

US-10-122-630-6
; Sequence 6, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.4e+08; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 1 CATAC 5

RESULT 3

US-10-122-633-4/c
; Sequence 4, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-4

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.4e+08; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 5 CATAC 1

RESULT 4

US-10-122-633-6
; Sequence 6, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.4e+08; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5
|||||
Db 1 CATAC 5

RESULT 5

US-10-027-632-178029
; Sequence 178029, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 178029
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-178029

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Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
        |||||
Db      1 CATAC 5

RESULT 6
US-10-027-632-178043
; Sequence 178043, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178043
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-178043

Query Match      100.0%; Score 5; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
        |||||
Db      1 CATAC 5

RESULT 7
US-10-122-630-3/c
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; GENERAL INFORMATION:
; RESULT 9
US-10-122-633-3/c
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
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; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
; US-10-122-630-3

Query Match      100.0%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
        |||||
Db      6 CATAC 2

RESULT 8
US-10-122-630-7/c
; Sequence 7, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
; US-10-122-630-7

Query Match      100.0%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
        |||||
Db      6 CATAC 2

RESULT 9
US-10-122-633-3/c
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
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; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match 100.0%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 6 CATAC 2

RESULT 10
US-10-122-633-7/c
; Sequence 7, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

Query Match 100.0%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 6 CATAC 2

RESULT 11
US-10-027-632-178029
; Sequence 178029, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178029
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029

Query Match 100.0%; Score 5; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db 1 CATAC 5

RESULT 12
US-10-027-632-178043
; Sequence 178043, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178043
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178043

Query Match 100.0%; Score 5; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

RESULT 13
US-09-142-593-11
; Sequence 11, Application US/09142593
; Patent No. US20020016975A1
; GENERAL INFORMATION:
; APPLICANT: HACKETT ET AL.
; TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
; INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,593
; FILING DATE: 10-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/040,664
; FILING DATE: 11-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,868
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/065,303
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04687
; FILING DATE: 11-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 110.00450101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-142-593-11

Query Match 100.0%; Score 5; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.9e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 2 CATAC 6

RESULT 14
US-09-927-886-17
; Sequence 17, Application US/09927886
; Patent No. US20020103152A1
; GENERAL INFORMATION:
; APPLICANT: Kay, Mark A.

; APPLICANT: Yant, Stephen
; TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
; FILE REFERENCE: STAN-160CIP
; CURRENT APPLICATION NUMBER: US/09/927,886
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/162,279
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 09/440,301
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: transposon repeat sequence
US-09-927-886-17

Query Match 100.0%; Score 5; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.9e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 2 CATAC 6

RESULT 15
US-09-861-014-6
; Sequence 6, Application US/09861014
; Patent No. US20020115216A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Clifford
; APPLICANT: Kren, Betsy
; APPLICANT: Linehan-Stieers, Cheryle
; APPLICANT: McIvor, R.
; APPLICANT: Hackett, Perry
; TITLE OF INVENTION: Composition for Delivery of Compounds to Cells
; FILE REFERENCE: 110.01330101
; CURRENT APPLICATION NUMBER: US/09/861,014
; CURRENT FILING DATE: 2001-05-19
; PRIOR APPLICATION NUMBER: US 60/206,002
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/285,121
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Direct repeat sequence
US-09-861-014-6

Query Match 100.0%; Score 5; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.9e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 2 CATAC 6

Search completed: August 11, 2004, 21:11:06
Job time : 73.4301 secs

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